

SEQUENCE LISTING

<110> Reinhard, Christoph
Jefferson, Anne B.
Chan, Vivien W.

<120> TTK in Diagnosis and as a Therapeutic
Target in Cancer

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<150> 60/289,813
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aac tcg gga act gtt aac caa att atg atg atg gca aac aac cca gag 1166
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 Glu Ala Leu Pro Pro Asp Lys Tyr Gly Gln Asn Glu Ser Phe Ala Arg
 80 85 90 95

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 Ala Arg Asp Tyr Phe Gln Met Ala Arg Ala Asn Cys Lys Lys Phe Ala
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 Pro Leu Glu Met Leu Glu Ile Ala Leu Arg Asn Leu Asn Leu Gln Lys
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Val Asp Gly Met Leu Lys Leu Ile Asp Phe Gly Ile Ala Asn Gln Met			
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caa cca gat aca aca agt gtt aaa gat tct cag gtt ggc aca gtt			3038
Gln Pro Asp Thr Thr Ser Val Val Lys Asp Ser Gln Val Gly Thr Val			
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Asn Tyr Met Pro Pro Glu Ala Ile Lys Asp Met Ser Ser Arg Glu			
675	680	685	
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Gln Ile Ile Asn Gln Ile Ser Lys Leu His Ala Ile Ile Asp Pro Asn			
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cat gaa att gaa ttt ccc gat att cca gag aaa gat ctt caa gat gtg			3278
His Glu Ile Glu Phe Pro Asp Ile Pro Glu Lys Asp Leu Gln Asp Val			
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tta aag tgt tgt tta aaa agg gac cca aaa cag agg ata tcc att cct			3326
Leu Lys Cys Cys Leu Lys Arg Asp Pro Lys Gln Arg Ile Ser Ile Pro			
755	760	765	
gag ctc ctg gct cat cca tat gtt caa att caa act cat cca gtt aac			3374
Glu Leu Leu Ala His Pro Tyr Val Gln Ile Gln Thr His Pro Val Asn			
770	775	780	
caa atg gcc aag gga acc act gaa gaa atg aaa tat gtt ctg ggc caa			3422
Gln Met Ala Lys Gly Thr Thr Glu Glu Met Lys Tyr Val Leu Gly Gln			
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835	840		
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Ala Leu Pro Pro Asp Lys Tyr Gly Gln Asn Glu Ser Phe Ala Arg Ile
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Arg Asp Tyr Phe Gln Met Ala Arg Ala Asn Cys Lys Lys Phe Ala Phe
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Lys Ser Lys Gln Leu Leu Lys Ala Val Glu Arg Gly Ala Val Pro
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Lys Gln Trp Gln Ala Lys Arg Lys Ser Glu Cys Ile Asn Gln Asn Pro

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Asp Asn Gln Thr Leu Asp Ser Tyr Arg Asn Glu Ile Ala Tyr Leu Asn		
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Lys Leu Gln Gln His Ser Asp Lys Ile Ile Arg Leu Tyr Asp Tyr Glu		
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Ile Thr Asp Gln Tyr Ile Tyr Met Val Met Glu Cys Gly Asn Ile Asp		
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Lys Cys Cys Leu Lys Arg Asp Pro Lys Gln Arg Ile Ser Ile Pro Glu		
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Met Ala Lys Gly Thr Thr Glu Glu Met Lys Tyr Val Leu Gly Gln Leu		
785	790	795
Val Gly Leu Asn Ser Pro Asn Ser Ile Leu Lys Ala Ala Lys Thr Leu		
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Tyr Glu His Tyr Ser Gly Gly Glu Ser His Asn Ser Ser Ser Ser Lys		
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Thr Phe Glu Lys Lys Arg Gly Lys Lys
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Ile Asp Glu Val Val Gly Gln Gly Ala Phe Ala Thr Val Lys Lys Ala			
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Ile Glu Arg Thr Thr Gly Lys Thr Phe Ala Val Lys Ile Ile Ser Lys			
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265	270	275	
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Asp Leu Met Asp Phe Val Ala Ala His Gly Ala Val Gly Glu Asp Ala			
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Gly Arg Glu Ile Ser Arg Gln Ile Leu Thr Ala Ile Lys Tyr Ile His			
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Ser Met Gly Ile Ser His Arg Asp Leu Lys Pro Asp Asn Ile Leu Ile			
315	320	325	
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Pro Asp Glu Tyr Glu Glu Arg Asn Glu Tyr Ser Ser Leu Val Asp Met			
380	385	390	

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cag gat cag gaa gac caa gat gga aaa att caa gga ttt aaa ata ccc Gln Asp Gln Glu Asp Gln Asp Gly Lys Ile Gln Gly Phe Lys Ile Pro 520 525 530 535	1638
gca cac gcc cct att cga tat aca caaaa gac att gaa gca gaa Ala His Ala Pro Ile Arg Tyr Thr Gln Pro Lys Ser Ile Glu Ala Glu 540 545 550	1686
act aga gaa caa aaa ctt tta cat tcc aat aat act gag aat gtc aag Thr Arg Glu Gln Lys Leu Leu His Ser Asn Asn Thr Glu Asn Val Lys 555 560 565	1734
agc tca aag aaa aag ggt aat ggt agg ttt tta act tta aaa cca ttg Ser Ser Lys Lys Gly Asn Gly Arg Phe Leu Thr Leu Lys Pro Leu 570 575 580	1782
cct gac agc att att caa gaa agc ctg gag att cag caa ggt gtg aat Pro Asp Ser Ile Ile Gln Glu Ser Leu Glu Ile Gln Gln Gly Val Asn 585 590 595	1830
cca ttt ttc att ggt aga tcc gag gat tgc aat tgt aaa att gaa gac Pro Phe Phe Ile Gly Arg Ser Glu Asp Cys Asn Cys Lys Ile Glu Asp 600 605 610 615	1878
aat agg ttg tct cga gtt cat tgc ttc att ttc aaa aag agg cat gct	1926

Asn Arg Leu Ser Arg Val His Cys Phe Ile Phe Lys Lys Arg His Ala			
620	625	630	
gta ggc aaa agc atg tat gaa tct ccg gca caa ggt tta gat gat att			1974
Val Gly Lys Ser Met Tyr Glu Ser Pro Ala Gln Gly Leu Asp Asp Ile			
635	640	645	
tgg tat tgc cac acc gga act aac gtg agc tat tta aat aat aac cgc			2022
Trp Tyr Cys His Thr Gly Thr Asn Val Ser Tyr Leu Asn Asn Asn Arg			
650	655	660	
atg ata cag ggt acg aaa ttc ctt tta caa gac gga gat gaa atc aag			2070
Met Ile Gln Gly Thr Lys Phe Leu Leu Gln Asp Gly Asp Glu Ile Lys			
665	670	675	
atc att tgg gat aaa aac aat aaa ttt gtc att ggc ttt aaa gtg gaa			2118
Ile Ile Trp Asp Lys Asn Asn Lys Phe Val Ile Gly Phe Lys Val Glu			
680	685	690	695
att aac gat act aca ggt ctg ttt aac gag gga tta ggt atg tta caa			2166
Ile Asn Asp Thr Thr Gly Leu Phe Asn Glu Gly Leu Gly Met Leu Gln			
700	705	710	
gaa caa aga gta gta ctt aag caa aca gcc gaa gaa aaa gat ttg gtg			2214
Glu Gln Arg Val Val Leu Lys Gln Thr Ala Glu Glu Lys Asp Leu Val			
715	720	725	
aaa aag tta acc cag atg atg gca gct caa cgt gca aat caa ccc tcg			2262
Lys Lys Leu Thr Gln Met Met Ala Ala Gln Arg Ala Asn Gln Pro Ser			
730	735	740	
gct tct tct tca tca atg tcg gct aag aag ccg cca gtt agc gat aca			2310
Ala Ser Ser Ser Met Ser Ala Lys Lys Pro Pro Val Ser Asp Thr			
745	750	755	
aat aat aac ggc aat aat tcg gta cta aac gac ttg gta gag tca ccg			2358
Asn Asn Asn Gly Asn Asn Ser Val Leu Asn Asp Leu Val Glu Ser Pro			
760	765	770	775
att aat gcg aat acg ggg aac att ttg aag aga ata cat tcg gta agt			2406
Ile Asn Ala Asn Thr Gly Asn Ile Leu Lys Arg Ile His Ser Val Ser			
780	785	790	
tta tcg caa tca caa att gat cct agt aag aag gtt aaa agg gca aaa			2454
Leu Ser Gln Ser Gln Ile Asp Pro Ser Lys Lys Val Lys Arg Ala Lys			
795	800	805	
ttg gac caa acc tca aaa ggc ccc gag aat ttg caa ttt tcg taa			2499
Leu Asp Gln Thr Ser Lys Gly Pro Glu Asn Leu Gln Phe Ser *			
810	815	820	
ccaaggacaa atacccatag aaaatgctgc cccttttaa gagagaagat ggtagataacc	2559		
aataactcaga attcccagta caaagaacca atatcgagt caataaacag tatgtatgaaac	2619		
ttgcttcgc aaataaaaaga tatcactcag aagcacccag taataaagga tgcagatagc	2679		
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<212> PRT
<213> *Saccharomyces cerevisiae*

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Val Cys Arg Val Ile Cys Thr Thr Gly Gln Ile Pro Ile Arg Asp Leu
35 40 45
Ser Ala Asp Ile Ser Gln Val Leu Lys Glu Lys Arg Ser Ile Lys Lys
50 55 60
Val Trp Thr Phe Gly Arg Asn Pro Ala Cys Asp Tyr His Leu Gly Asn
65 70 75 80
Ile Ser Arg Leu Ser Asn Lys His Phe Gln Ile Leu Leu Gly Glu Asp
85 90 95
Gly Asn Leu Leu Asn Asp Ile Ser Thr Asn Gly Thr Trp Leu Asn
100 105 110
Gly Gln Lys Val Glu Lys Asn Ser Asn Gln Leu Leu Ser Gln Gly Asp
115 120 125
Glu Ile Thr Val Gly Val Gly Val Glu Ser Asp Ile Leu Ser Leu Val
130 135 140
Ile Phe Ile Asn Asp Lys Phe Lys Gln Cys Leu Glu Gln Asn Lys Val
145 150 155 160
Asp Arg Ile Arg Ser Asn Leu Lys Asn Thr Ser Lys Ile Ala Ser Pro
165 170 175
Gly Leu Thr Ser Ser Thr Ala Ser Ser Met Val Ala Asn Lys Thr Gly
180 185 190
Ile Phe Lys Asp Phe Ser Ile Ile Asp Glu Val Val Gly Gln Gly Ala
195 200 205
Phe Ala Thr Val Lys Lys Ala Ile Glu Arg Thr Thr Gly Lys Thr Phe
210 215 220
Ala Val Lys Ile Ile Ser Lys Arg Lys Val Ile Gly Asn Met Asp Gly
225 230 235 240
Val Thr Arg Glu Leu Glu Val Leu Gln Lys Leu Asn His Pro Arg Ile
245 250 255
Val Arg Leu Lys Gly Phe Tyr Glu Asp Thr Glu Ser Tyr Tyr Met Val
260 265 270
Met Glu Phe Val Ser Gly Gly Asp Leu Met Asp Phe Val Ala Ala His
275 280 285
Gly Ala Val Gly Glu Asp Ala Gly Arg Glu Ile Ser Arg Gln Ile Leu
290 295 300
Thr Ala Ile Lys Tyr Ile His Ser Met Gly Ile Ser His Arg Asp Leu
305 310 315 320
Lys Pro Asp Asn Ile Leu Ile Glu Gln Asp Asp Pro Val Leu Val Lys
325 330 335
Ile Thr Asp Phe Gly Leu Ala Lys Val Gln Gly Asn Gly Ser Phe Met
340 345 350
Lys Thr Phe Cys Gly Thr Leu Ala Tyr Val Ala Pro Glu Val Ile Arg
355 360 365
Gly Lys Asp Thr Ser Val Ser Pro Asp Glu Tyr Glu Glu Arg Asn Glu
370 375 380
Tyr Ser Ser Leu Val Asp Met Trp Ser Met Gly Cys Leu Val Tyr Val
385 390 395 400
Ile Leu Thr Gly His Leu Pro Phe Ser Gly Ser Thr Gln Asp Gln Leu
405 410 415

Tyr Lys Gln Ile Gly Arg Gly Ser Tyr His Glu Gly Pro Leu Lys Asp
 420 425 430
 Phe Arg Ile Ser Glu Glu Ala Arg Asp Phe Ile Asp Ser Leu Leu Gln
 435 440 445
 Val Asp Pro Asn Asn Arg Ser Thr Ala Ala Lys Ala Leu Asn His Pro
 450 455 460
 Trp Ile Lys Met Ser Pro Leu Gly Ser Gln Ser Tyr Gly Asp Phe Ser
 465 470 475 480
 Gln Ile Ser Leu Ser Gln Ser Leu Ser Gln Gln Lys Leu Leu Glu Asn
 485 490 495
 Met Asp Asp Ala Gln Tyr Glu Phe Val Lys Ala Gln Arg Lys Leu Gln
 500 505 510
 Met Glu Gln Gln Leu Gln Glu Gln Asp Gln Glu Asp Gln Asp Gly Lys
 515 520 525
 Ile Gln Gly Phe Lys Ile Pro Ala His Ala Pro Ile Arg Tyr Thr Gln
 530 535 540
 Pro Lys Ser Ile Glu Ala Glu Thr Arg Glu Gln Lys Leu Leu His Ser
 545 550 555 560
 Asn Asn Thr Glu Asn Val Lys Ser Ser Lys Lys Lys Gly Asn Gly Arg
 565 570 575
 Phe Leu Thr Leu Lys Pro Leu Pro Asp Ser Ile Ile Gln Glu Ser Leu
 580 585 590
 Glu Ile Gln Gln Gly Val Asn Pro Phe Phe Ile Gly Arg Ser Glu Asp
 595 600 605
 Cys Asn Cys Lys Ile Glu Asp Asn Arg Leu Ser Arg Val His Cys Phe
 610 615 620
 Ile Phe Lys Lys Arg His Ala Val Gly Lys Ser Met Tyr Glu Ser Pro
 625 630 635 640
 Ala Gln Gly Leu Asp Asp Ile Trp Tyr Cys His Thr Gly Thr Asn Val
 645 650 655
 Ser Tyr Leu Asn Asn Asn Arg Met Ile Gln Gly Thr Lys Phe Leu Leu
 660 665 670
 Gln Asp Gly Asp Glu Ile Lys Ile Ile Trp Asp Lys Asn Asn Lys Phe
 675 680 685
 Val Ile Gly Phe Lys Val Glu Ile Asn Asp Thr Thr Gly Leu Phe Asn
 690 695 700
 Glu Gly Leu Gly Met Leu Gln Glu Gln Arg Val Val Leu Lys Gln Thr
 705 710 715 720
 Ala Glu Glu Lys Asp Leu Val Lys Lys Leu Thr Gln Met Met Ala Ala
 725 730 735
 Gln Arg Ala Asn Gln Pro Ser Ala Ser Ser Ser Met Ser Ala Lys
 740 745 750
 Lys Pro Pro Val Ser Asp Thr Asn Asn Asn Gly Asn Asn Ser Val Leu
 755 760 765
 Asn Asp Leu Val Glu Ser Pro Ile Asn Ala Asn Thr Gly Asn Ile Leu
 770 775 780
 Lys Arg Ile His Ser Val Ser Leu Ser Gln Ser Gln Ile Asp Pro Ser
 785 790 795 800
 Lys Lys Val Lys Arg Ala Lys Leu Asp Gln Thr Ser Lys Gly Pro Glu
 805 810 815
 Asn Leu Gln Phe Ser
 820

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<213> Homo sapiens

<220>

<221> CDS

<222> (289) ... (1230)

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ctgccccacc ccgctggcgc gcccctccgc cgccagtccc ggcagcgcgc tcagttgtcc 120
tccgactcgc cctcggcctt ccgcgccagc cgcagccaca gcccgaacgc caccgcgc 180
cacagccaca gccacagccc caggcatagc cttcggcaca gccccggctc cggctcctgc 240
ggcagtcctt ctgggcaccc tccctgcgcc gacatcctgg aggttggg atg ctc ttg 297

Met Leu Leu

1

tcc aaa atc aac tcg ctt gcc cac ctg cgc gcc gcg ccc tgc aac gac 345
Ser Lys Ile Asn Ser Leu Ala His Leu Arg Ala Ala Pro Cys Asn Asp
5 10 15

ctg cac gcc acc aag ctg gcg ccc ggc aag gag aag gag ccc ctg gag 393
Leu His Ala Thr Lys Leu Ala Pro Gly Lys Glu Lys Glu Pro Leu Glu
20 25 30 35

tcg cag tac cag gtg ggc ccg cta ctg ggc agc ggc ttc ggc tcg 441
Ser Gln Tyr Gln Val Gly Pro Leu Leu Gly Ser Gly Gly Phe Gly Ser
40 45 50

gtc tac tca ggc atc cgc gtc tcc gac aac ttg ccg gtg gcc atc aaa 489
Val Tyr Ser Gly Ile Arg Val Ser Asp Asn Leu Pro Val Ala Ile Lys
55 60 65

cac gtg gag aag gac ccg att tcc gac tgg gga gag ctg cct aat ggc 537
His Val Glu Lys Asp Arg Ile Ser Asp Trp Gly Glu Leu Pro Asn Gly
70 75 80

act cga gtg ccc atg gaa gtg gtc ctg ctg aag aag gtg agc tcg ggt 585
Thr Arg Val Pro Met Glu Val Val Leu Leu Lys Lys Val Ser Ser Gly
85 90 95

ttc tcc ggc gtc att agg ctc ctg gac tgg ttc gag agg ccc gac agt 633
Phe Ser Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Arg Pro Asp Ser
100 105 110 115

ttc gtc ctg atc ctg gag agg ccc gag ccg gtg caa gat ctc ttc gac 681
Phe Val Leu Ile Leu Glu Arg Pro Glu Pro Val Gln Asp Leu Phe Asp
120 125 130

ttc atc acg gaa agg gga gcc ctg caa gag gag ctc gcc cgc agc ttc 729
Phe Ile Thr Glu Arg Gly Ala Leu Gln Glu Leu Ala Arg Ser Phe
135 140 145

ttc tgg cag gtg ctg gag gcc gtg cgg cac tgc cac aac tgc ggg gtg 777
Phe Trp Gln Val Leu Glu Ala Val Arg His Cys His Asn Cys Gly Val
150 155 160

ctc cac cgc gac atc aag gac gaa aac atc ctt atc gac ctc aat cgc 825
Leu His Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp Leu Asn Arg

165

170

175

ggc gag ctc aag ctc atc gac ttc ggg tcg ggg gcg ctg ctc aaa gac			873
Gly Glu Leu Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp			
180	185	190	195
acc gtc tac acg gac ttc gat ggg acc cga gtg tat agc cct cca gag			921
Thr Val Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu			
200	205	210	
tgg atc cgc tac cat cgc tac cat ggc agg tcg gcg gca gtc tgg tcc			969
Trp Ile Arg Tyr His Arg Tyr His Gly Arg Ser Ala Ala Val Trp Ser			
215	220	225	
ctg ggg atc ctg ctg tat gat atg gtg tgt gga gat att cct ttc gag			1017
Leu Gly Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile Pro Phe Glu			
230	235	240	
cat gac gaa gag atc atc agg ggc cag gtt ttc ttc agg cag agg gtc			1065
His Asp Glu Glu Ile Ile Arg Gly Gln Val Phe Phe Arg Gln Arg Val			
245	250	255	
tct tca gaa tgt cag cat ctc att aga tgg tgc ttg gcc ctg aga cca			1113
Ser Ser Glu Cys Gln His Leu Ile Arg Trp Cys Leu Ala Leu Arg Pro			
260	265	270	275
tca gat agg cca acc ttc gaa gaa atc cag aac cat cca tgg atg caa			1161
Ser Asp Arg Pro Thr Phe Glu Glu Ile Gln Asn His Pro Trp Met Gln			
280	285	290	
gat gtt ctc ctg ccc cag gaa act gct gag atc cac ctc cac agc ctg			1209
Asp Val Leu Leu Pro Gln Glu Thr Ala Glu Ile His Leu His Ser Leu			
295	300	305	
tcg ccg ggg ccc agc aaa tag cagccttctt ggcaggcctt cccctcttctt			1260
Ser Pro Gly Pro Ser Lys *			
310			
gtcagatgcc cgagggaggg gaaggttctg tctccagtt cccgagtacc agtgacacgt			1320
ctcgccaagc aggacagtgc ttgatacagg aacaacattt acaactcatt ccagatccca			1380
ggcccttggaa gcgtccccc caacagttagt gaaaggatggc tctccagggg tccttaggcct			1440
caactccctcc catagataact ctcttcttctt cataggtgtc cagcattgtt ggactgtga			1500
aatatccccgg ggggtgggggg tgggggtggg tcagaaccct gccatggAAC tgtttccccc			1560
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actgtttcaa agccaaagacc tcacacacag aaaaaatgca caaacaaatgc aatcaacaga			1980
aaagctgtaa atgtgtgtac agtggcatg gtatgtataca aaaagattgt agtggatcta			2040
atttttcaga aattttgcct ttaagttatt ttacctgtt ttgtttcttg ttttgaagaaga			2100
tgcgcattct aacctggagg tcaatgttat gtatTTTATTt atttattttat ttgggttccct			2160
tccttattcca agcttccata gctgtgtccc tagttttctt tcctccccc ctcctctgac			2220
ttggggacct tttggggggag ggctgcgacg cttgtctgt ttgtgggggt acgggactca			2280
ggcgggacag tgctgcagct ccctggcttc tttttttttttt ctcacacact tacccaggtg			2340
ggtcccggtc ctgtgggtga tggggagggg cattgtgtac tgtgtatata ggataattat			2400

gaaaaggcagt tctggatggt gtgccttcca gatcctctct ggggctgtgt tttgagcagc 2460
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<212> PRT
<213> Homo sapiens

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Cys Asn Asp Leu His Ala Thr Lys Leu Ala Pro Gly Lys Glu Lys Glu
20 25 30
Pro Leu Glu Ser Gln Tyr Gln Val Gly Pro Leu Leu Gly Ser Gly Gly
35 40 45
Phe Gly Ser Val Tyr Ser Gly Ile Arg Val Ser Asp Asn Leu Pro Val
50 55 60
Ala Ile Lys His Val Glu Lys Asp Arg Ile Ser Asp Trp Gly Glu Leu
65 70 75 80
Pro Asn Gly Thr Arg Val Pro Met Glu Val Val Leu Leu Lys Lys Val
85 90 95
Ser Ser Gly Phe Ser Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Arg
100 105 110
Pro Asp Ser Phe Val Leu Ile Leu Glu Arg Pro Glu Pro Val Gln Asp
115 120 125
Leu Phe Asp Phe Ile Thr Glu Arg Gly Ala Leu Gln Glu Glu Leu Ala
130 135 140
Arg Ser Phe Phe Trp Gln Val Leu Glu Ala Val Arg His Cys His Asn
145 150 155 160
Cys Gly Val Leu His Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp
165 170 175
Leu Asn Arg Gly Glu Leu Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu
180 185 190
Leu Lys Asp Thr Val Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser
195 200 205
Pro Pro Glu Trp Ile Arg Tyr His Arg Tyr His Gly Arg Ser Ala Ala
210 215 220
Val Trp Ser Leu Gly Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile
225 230 235 240
Pro Phe Glu His Asp Glu Glu Ile Ile Arg Gly Gln Val Phe Phe Arg
245 250 255
Gln Arg Val Ser Ser Glu Cys Gln His Leu Ile Arg Trp Cys Leu Ala
260 265 270
Leu Arg Pro Ser Asp Arg Pro Thr Phe Glu Glu Ile Gln Asn His Pro
275 280 285
Trp Met Gln Asp Val Leu Leu Pro Gln Glu Thr Ala Glu Ile His Leu
290 295 300
His Ser Leu Ser Pro Gly Pro Ser Lys
305 310

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<222> (789) ... (2795)

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tctatATTTG attaatCTCT tgTTatCTTG gtGATGATCG cacaAGTATG tactCCTGTA 180
tctgcaagaa tatCTGTTT aaACTTTCA aAGCAAGGAA accCCGTCTT atATAGGTTA 240
tccgcaagg tcacatTTTC ttGCAAATAG aAGAAAAGC acccacaAGC acactAACAC 300
agtGCCAGAG caaaaACTATA tcCTTGCAT ccGATCTCAA acGCTGTTCT tatCGCATCT 360
gtCTTGTGTC ttTCATCTGC attTACCTT TCTTTTcat CCTCTATTG CCTTTTCATT 420
agtGGCAATT ttTCCAGTT ttTCCCTCTG CGTCCC GTT GACCTGAAAG GATCTTCTA 480
acgtGTGTTG tCTACTAGTG agCGATTG TGAGCCATAC acGTTCTATA gAAAATTGAA 540
taaACTTTAC ttCAAAGGGAA tCTGGACACA gagATAACTG cttACCTGCT tGCCGGAAAGA 600
aaAGAAATTAC taaaaAAAGGAA gacaAGGGTA gCTGCTATTG tGGGTACACG tttcacAGAA 660
ctACTTTTC ctGTGCTTC tCCAGACATC AACGTCTAC aactAAACT gataAAAGTAC 720
ccGTTTTCC gtACATTTCT atAGATACAT TATTATATA AGCAGATCGA GACGTTAATT 780
tctcaaAG atG gaa gac aag ttt gct aac ctc agt ctc cat gag aaa act 830
Met Glu Asp Lys Phe Ala Asn Leu Ser Leu His Glu Lys Thr
1 5 10

ggt aag tca tct atc caa tta aac gag caa aca ggc tca gat aat ggc 878
Gly Lys Ser Ser Ile Gln Leu Asn Glu Gln Thr Gly Ser Asp Asn Gly
15 20 25 30

tct gct gtc aag aga aca tct tcg acg tcc tcg cac tac aat aac atc 926
Ser Ala Val Lys Arg Thr Ser Ser Thr Ser His Tyr Asn Asn Ile
35 40 45

aac gct gac ctt cat gct cgt gta aaa gct ttt caa gaa caa cgt gca 974
Asn Ala Asp Leu His Ala Arg Val Lys Ala Phe Gln Glu Gln Arg Ala
50 55 60

ttg aaa agg tct gcc agc gtg ggc agt aat caa agc gag caa gac aaa 1022
Leu Lys Arg Ser Ala Ser Val Gly Ser Asn Gln Ser Glu Gln Asp Lys
65 70 75

ggc agt tca caa tca cct aaa cat att cag cag att gtt aat aag cca 1070
Gly Ser Ser Gln Ser Pro Lys His Ile Gln Gln Ile Val Asn Lys Pro
80 85 90

ttg ccg cct ctt ccc gta gca gga agt tct aag gtt tca caa aga atg 1118
Leu Pro Pro Leu Pro Val Ala Gly Ser Ser Lys Val Ser Gln Arg Met
95 100 105 110

agt agc caa gtc gtg caa gcg tcc aag agc act ctt aag aac gtt 1166
Ser Ser Gln Val Val Gln Ala Ser Ser Lys Ser Thr Leu Lys Asn Val
115 120 125

ctg gac aat caa gaa aca caa aac att acc gac gta aat att aac atc 1214
Leu Asp Asn Gln Glu Thr Gln Asn Ile Thr Asp Val Asn Ile Asn Ile
130 135 140

gat aca acc aaa att acc gcc aca aca att ggt gta aat act ggc cta 1262
Asp Thr Thr Lys Ile Thr Ala Thr Thr Ile Gly Val Asn Thr Gly Leu
145 150 155

cct gct act gac att acg ccg tca gtt tct aat act gca tca gca aca Pro Ala Thr Asp Ile Thr Pro Ser Val Ser Asn Thr Ala Ser Ala Thr	160 165 170	1310
cat aag gcg caa ttg ctg aat cct aac aga agg gca cca aga agg ccg His Lys Ala Gln Leu Leu Asn Pro Asn Arg Arg Ala Pro Arg Arg Pro	175 180 185 190	1358
ctt tct acc cag cac cct aca aga cca aat gtt gcc ccg cat aag gcc Leu Ser Thr Gln His Pro Thr Arg Pro Asn Val Ala Pro His Lys Ala	195 200 205	1406
cct gct ata atc aac aca cca aaa caa agt tta agt gcc cgt cga ggg Pro Ala Ile Ile Asn Thr Pro Lys Gln Ser Leu Ser Ala Arg Arg Gly	210 215 220	1454
ctc aaa tta cca cca gga gga atg tca tta aaa atg ccc act aaa aca Leu Lys Leu Pro Pro Gly Gly Met Ser Leu Lys Met Pro Thr Lys Thr	225 230 235	1502
gct caa cag ccg cag cag ttt gcc cca agc cct tca aac aaa aaa cat Ala Gln Gln Pro Gln Gln Phe Ala Pro Ser Pro Ser Asn Lys Lys His	240 245 250	1550
ata gaa acc tta tca aac agc aaa gtt gtt gaa ggg aaa aga tcg aat Ile Glu Thr Leu Ser Asn Ser Lys Val Val Glu Gly Lys Arg Ser Asn	255 260 265 270	1598
ccg ggt tct ttg ata aat ggt gtg caa agc aca tcc acc tca tca agt Pro Gly Ser Leu Ile Asn Gly Val Gln Ser Thr Ser Thr Ser Ser	275 280 285	1646
acc gaa ggc cca cat gac act gta ggc act aca ccc aga act gga aac Thr Glu Gly Pro His Asp Thr Val Gly Thr Thr Pro Arg Thr Gly Asn	290 295 300	1694
agc aac aac tct tca aat tct ggt agt agt ggt ggt ggt ctt ttc Ser Asn Asn Ser Ser Asn Ser Gly Ser Ser Gly Gly Gly Leu Phe	305 310 315	1742
gca aat ttc tcg aaa tac gtg gat atc aaa tcc ggc tct ttg aat ttt Ala Asn Phe Ser Lys Tyr Val Asp Ile Lys Ser Gly Ser Leu Asn Phe	320 325 330	1790
gca ggc aaa cta tcg cta tcc tct aaa gga ata gat ttc agc aat ggt Ala Gly Lys Leu Ser Leu Ser Ser Lys Gly Ile Asp Phe Ser Asn Gly	335 340 345 350	1838
tct agt tcg aga att aca ttg gac gaa cta gaa ttt ttg gat gaa ctg Ser Ser Ser Arg Ile Thr Leu Asp Glu Leu Glu Phe Leu Asp Glu Leu	355 360 365	1886
ggt cat ggt aac tat ggt aac gtc tca aag gta ctg cat aag ccc aca Gly His Gly Asn Tyr Gly Asn Val Ser Lys Val Leu His Lys Pro Thr	370 375 380	1934

aat gtt att atg gcg acg aag gaa gtc cgt ttg gag cta gat gag gct Asn Val Ile Met Ala Thr Lys Glu Val Arg Leu Glu Leu Asp Glu Ala	385	390	395	1982
aaa ttt aga caa att tta atg gaa cta gaa gtt ttg cat aaa tgc aat Lys Phe Arg Gln Ile Leu Met Glu Leu Glu Val Leu His Lys Cys Asn	400	405	410	2030
tct ccc tat att gtg gat ttt tat ggt gca ttc ttt att gag ggc gcc Ser Pro Tyr Ile Val Asp Phe Tyr Gly Ala Phe Phe Ile Glu Gly Ala	415	420	425	2078
415	420	425	430	
gtc tac atg tgt atg gaa tac atg gat ggt ggt tcc ttg gat aaa ata Val Tyr Met Cys Met Glu Tyr Met Asp Gly Gly Ser Leu Asp Lys Ile	435	440	445	2126
Tyr Asp Glu Ser Ser Glu Ile Gly Gly Ile Asp Glu Pro Gln Leu Ala	450	455	460	2174
450	455	460		
ttt att gcc aat gct gtc att cat gga cta aaa gaa ctc aaa gag cag Phe Ile Ala Asn Ala Val Ile His Gly Leu Lys Glu Leu Lys Glu Gln	465	470	475	2222
465	470	475		
cat aat atc ata cac aga gat gtc aaa cca aca aat att tta tgt tca His Asn Ile Ile His Arg Asp Val Lys Pro Thr Asn Ile Leu Cys Ser	480	485	490	2270
480	485	490		
gcc aac caa ggc acc gta aag ctg tgc gat ttc ggt gtt tct ggt aat Ala Asn Gln Gly Thr Val Lys Leu Cys Asp Phe Gly Val Ser Gly Asn	495	500	505	2318
495	500	505	510	
ttg gtg gca tct tta gcg aag act aat att ggt tgt cag tca tac atg Leu Val Ala Ser Leu Ala Lys Thr Asn Ile Gly Cys Gln Ser Tyr Met	515	520	525	2366
515	520	525		
gca cct gaa cga atc aaa tcg ttg aat cca gat aga gcc acc tat acc Ala Pro Glu Arg Ile Lys Ser Leu Asn Pro Asp Arg Ala Thr Tyr Thr	530	535	540	2414
530	535	540		
gta cag tca gac atc tgg tct tta ggt tta agc att ctg gaa atg gca Val Gln Ser Asp Ile Trp Ser Leu Gly Leu Ser Ile Leu Glu Met Ala	545	550	555	2462
545	550	555		
cta ggt aga tat ccg tat cca cca gaa aca tac gac aac att ttc tct Leu Gly Arg Tyr Pro Tyr Pro Pro Glu Thr Tyr Asp Asn Ile Phe Ser	560	565	570	2510
560	565	570		
caa ttg agc gct att gtt gat ggg ccg cca ccg aga tta cct tca gat Gln Leu Ser Ala Ile Val Asp Gly Pro Pro Arg Leu Pro Ser Asp	575	580	585	2558
575	580	585	590	
aaa ttc agt tct gac gca caa gat ttt gtt tct tta tgt cta caa aag Lys Phe Ser Ser Asp Ala Gln Asp Phe Val Ser Leu Cys Leu Gln Lys	595	600	605	2606
595	600	605		
att ccg gaa aga aga cct aca tac gca gct tta aca gag cat cct tgg				2654

Ile Pro Glu Arg Arg Pro Thr Tyr Ala Ala Leu Thr Glu His Pro Trp			
610	615	620	
tta gta aaa tac aga aac cag gat gtc cac atg agt gag tat atc act			2702
Leu Val Lys Tyr Arg Asn Gln Asp Val His Met Ser Glu Tyr Ile Thr			
625	630	635	
gaa cga tta gaa agg cgc aac aaa atc tta cg gaa cgt ggt gag aat			2750
Glu Arg Leu Glu Arg Arg Asn Lys Ile Leu Arg Glu Arg Gly Glu Asn			
640	645	650	
ggt tta tct aaa aat gta ccg gca tta cat atg ggt ggt tta tag			2795
Gly Leu Ser Lys Asn Val Pro Ala Leu His Met Gly Gly Leu *			
655	660	665	
cgttaatatac caaataaaaag caaacaggca cgtgaatata acaacaaaaaa aaaagcagac			2855
gaaaagctac tgtggaaatg atgcggcgaa tacaaaaaaaaa ccttacatat acatatgttt			2915
attgtataaa acttgcatta tactcggtt agacatataat atatataat attcatataat			2975
atataatcgctc tgacttcctt ttgtcgaacc taaaaaaaaaggg cacgaattat gacagagtat			3035
tgaggggatg ttatttcaag caccggcaag tgaagcgtatg tggacgtcaa tatattgtgt			3095
tattcgat tttgttacggc catcgactcc tcgaaattat ttacgttcgg ggctgacaac			3155
gcaagaaaaga aaaaatgctc tgaaattgtc tgatggttt tccgctctt acggctcaag			3215
gctaggaaag aaaaaaaaaagt cccaaatcat cgagaaaaata aaaggtgttt taaaagttca			3275
aatccacgtt attgagagta gatgtggagt ctggaccagg aactataacct gtatcttacc			3335
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Ser Ser Ile Gln Leu Asn Glu Gln Thr Gly Ser Asp Asn Gly Ser Ala			
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Val Lys Arg Thr Ser Ser Thr Ser His Tyr Asn Asn Ile Asn Ala			
35 40 45			
Asp Leu His Ala Arg Val Lys Ala Phe Gln Glu Gln Arg Ala Leu Lys			
50 55 60			
Arg Ser Ala Ser Val Gly Ser Asn Gln Ser Glu Gln Asp Lys Gly Ser			
65 70 75 80			
Ser Gln Ser Pro Lys His Ile Gln Gln Ile Val Asn Lys Pro Leu Pro			
85 90 95			
Pro Leu Pro Val Ala Gly Ser Ser Lys Val Ser Gln Arg Met Ser Ser			
100 105 110			
Gln Val Val Gln Ala Ser Ser Lys Ser Thr Leu Lys Asn Val Leu Asp			
115 120 125			
Asn Gln Glu Thr Gln Asn Ile Thr Asp Val Asn Ile Asn Ile Asp Thr			
130 135 140			
Thr Lys Ile Thr Ala Thr Ile Gly Val Asn Thr Gly Leu Pro Ala			
145 150 155 160			
Thr Asp Ile Thr Pro Ser Val Ser Asn Thr Ala Ser Ala Thr His Lys			
165 170 175			
Ala Gln Leu Leu Asn Pro Asn Arg Arg Ala Pro Arg Arg Pro Leu Ser			
180 185 190			

Thr Gln His Pro Thr Arg Pro Asn Val Ala Pro His Lys Ala Pro Ala
 195 200 205
 Ile Ile Asn Thr Pro Lys Gln Ser Leu Ser Ala Arg Arg Gly Leu Lys
 210 215 220
 Leu Pro Pro Gly Gly Met Ser Leu Lys Met Pro Thr Lys Thr Ala Gln
 225 230 235 240
 Gln Pro Gln Gln Phe Ala Pro Ser Pro Ser Asn Lys Lys His Ile Glu
 245 250 255
 Thr Leu Ser Asn Ser Lys Val Val Glu Gly Lys Arg Ser Asn Pro Gly
 260 265 270
 Ser Leu Ile Asn Gly Val Gln Ser Thr Ser Thr Ser Ser Thr Glu
 275 280 285
 Gly Pro His Asp Thr Val Gly Thr Thr Pro Arg Thr Gly Asn Ser Asn
 290 295 300
 Asn Ser Ser Asn Ser Gly Ser Ser Gly Gly Gly Leu Phe Ala Asn
 305 310 315 320
 Phe Ser Lys Tyr Val Asp Ile Lys Ser Gly Ser Leu Asn Phe Ala Gly
 325 330 335
 Lys Leu Ser Leu Ser Ser Lys Gly Ile Asp Phe Ser Asn Gly Ser Ser
 340 345 350
 Ser Arg Ile Thr Leu Asp Glu Leu Glu Phe Leu Asp Glu Leu Gly His
 355 360 365
 Gly Asn Tyr Gly Asn Val Ser Lys Val Leu His Lys Pro Thr Asn Val
 370 375 380
 Ile Met Ala Thr Lys Glu Val Arg Leu Glu Leu Asp Glu Ala Lys Phe
 385 390 395 400
 Arg Gln Ile Leu Met Glu Leu Glu Val Leu His Lys Cys Asn Ser Pro
 405 410 415
 Tyr Ile Val Asp Phe Tyr Gly Ala Phe Phe Ile Glu Gly Ala Val Tyr
 420 425 430
 Met Cys Met Glu Tyr Met Asp Gly Gly Ser Leu Asp Lys Ile Tyr Asp
 435 440 445
 Glu Ser Ser Glu Ile Gly Gly Ile Asp Glu Pro Gln Leu Ala Phe Ile
 450 455 460
 Ala Asn Ala Val Ile His Gly Leu Lys Glu Leu Lys Glu Gln His Asn
 465 470 475 480
 Ile Ile His Arg Asp Val Lys Pro Thr Asn Ile Leu Cys Ser Ala Asn
 485 490 495
 Gln Gly Thr Val Lys Leu Cys Asp Phe Gly Val Ser Gly Asn Leu Val
 500 505 510
 Ala Ser Leu Ala Lys Thr Asn Ile Gly Cys Gln Ser Tyr Met Ala Pro
 515 520 525
 Glu Arg Ile Lys Ser Leu Asn Pro Asp Arg Ala Thr Tyr Thr Val Gln
 530 535 540
 Ser Asp Ile Trp Ser Leu Gly Leu Ser Ile Leu Glu Met Ala Leu Gly
 545 550 555 560
 Arg Tyr Pro Tyr Pro Pro Glu Thr Tyr Asp Asn Ile Phe Ser Gln Leu
 565 570 575
 Ser Ala Ile Val Asp Gly Pro Pro Arg Leu Pro Ser Asp Lys Phe
 580 585 590
 Ser Ser Asp Ala Gln Asp Phe Val Ser Leu Cys Leu Gln Lys Ile Pro
 595 600 605
 Glu Arg Arg Pro Thr Tyr Ala Ala Leu Thr Glu His Pro Trp Leu Val
 610 615 620
 Lys Tyr Arg Asn Gln Asp Val His Met Ser Glu Tyr Ile Thr Glu Arg
 625 630 635 640
 Leu Glu Arg Arg Asn Lys Ile Leu Arg Glu Arg Gly Glu Asn Gly Leu

645	650	655
Ser Lys Asn Val Pro Ala Leu His Met Gly Gly Leu		
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atg gcg gag cca gat ctg gag tgc gag cag atc cgt ctg aag tgt att	168	
Met Ala Pro Asp Leu Glu Cys Gln Ile Arg Leu Lys Cys Ile		
1	5	10
		15
cgt aag gag ggc ttc ttc acg gtg cct ccg gaa cac agg ctg gga cga	216	
Arg Lys Glu Gly Phe Phe Thr Val Pro Pro Glu His Arg Leu Gly Arg		
20	25	30
tgc cgg agt gtg aag gag ttt gag aag ctg aac cgc att gga gag ggt	264	
Cys Arg Ser Val Lys Glu Phe Glu Lys Leu Asn Arg Ile Gly Glu Gly		
35	40	45
acc tac ggc att gtg tat cgg gcc cgg gac acc cag aca gat gag att	312	
Thr Tyr Gly Ile Val Tyr Arg Ala Arg Asp Thr Gln Thr Asp Glu Ile		
50	55	60
gtc gca ctg aag aag gtg cgg atg gac aag gag aag gat ggc atc ccc	360	
Val Ala Leu Lys Lys Val Arg Met Asp Lys Glu Lys Asp Gly Ile Pro		
65	70	75
		80
atc agc agc ttg cgg gag atc acg ctg ctg ctc cgc ctg cgt cat ccg	408	
Ile Ser Ser Leu Arg Glu Ile Thr Leu Leu Arg Leu Arg His Pro		
85	90	95
aac atc gtg gag ctg aag gag gtg gtt gtg ggg aac cac ctg gag agc	456	
Asn Ile Val Glu Leu Lys Glu Val Val Val Gly Asn His Leu Glu Ser		
100	105	110
atc ttc ctg gtg atg ggt tac tgt gag cag gac ctg gcc agc ctc ctg	504	
Ile Phe Leu Val Met Gly Tyr Cys Glu Gln Asp Leu Ala Ser Leu Leu		
115	120	125
gag aat atg cca aca ccc ttc tcg gag gct cag gtc aag tgc atc gtg	552	
Glu Asn Met Pro Thr Pro Phe Ser Glu Ala Gln Val Lys Cys Ile Val		
130	135	140
ctg cag gtg ctc cgg ggc ctc cag tat ctg cac agg aac ttc att atc	600	
Leu Gln Val Leu Arg Gly Leu Gln Tyr Leu His Arg Asn Phe Ile Ile		
145	150	155
		160

cac agg gac ctg aag gtt tcc aac ttg ctc atg acc gac aag ggt tgt 648
 His Arg Asp Leu Lys Val Ser Asn Leu Leu Met Thr Asp Lys Gly Cys
 165 170 175

 gtg aag aca gcg gat ttc ggc ctg gcc cggttat ggt gtc cca gta 696
 Val Lys Thr Ala Asp Phe Gly Leu Ala Arg Ala Tyr Gly Val Pro Val
 180 185 190

 aag cca atg acc ccc aag gtg gtc act ctc tgg tac cga gcc cct gaa 744
 Lys Pro Met Thr Pro Lys Val Val Thr Leu Trp Tyr Arg Ala Pro Glu
 195 200 205

 ctg ctg ttg gga acc acc acg cag acc acc agc atc gac atg tgg gct 792
 Leu Leu Leu Gly Thr Thr Gln Thr Thr Ser Ile Asp Met Trp Ala
 210 215 220

 gtg ggc tgc ata ctg gcc gag ctg ctg gcg cac agg cct ctt ctc ccc 840
 Val Gly Cys Ile Leu Ala Glu Leu Leu Ala His Arg Pro Leu Leu Pro
 225 230 235 240

 ggc act tcc gag atc cac cag atc gac ttg atc gtg cag ctg ctg ggc 888
 Gly Thr Ser Glu Ile His Gln Ile Asp Leu Ile Val Gln Leu Leu Gly
 245 250 255

 acg ccc agt gag aac atc tgg ccg ggc ttt tcc aag ctg cca ctg gtc 936
 Thr Pro Ser Glu Asn Ile Trp Pro Gly Phe Ser Lys Leu Pro Leu Val
 260 265 270

 ggc cag tac agc ctc cgg aag cag ccc tac aac aac ctg aag cac aag 984
 Gly Gln Tyr Ser Leu Arg Lys Gln Pro Tyr Asn Asn Leu Lys His Lys
 275 280 285

 ttc cca tgg ctg tcg gag gcc ggg ctg cgc ctg ctg cac ttc ctg ttc 1032
 Phe Pro Trp Leu Ser Glu Ala Gly Leu Arg Leu Leu His Phe Leu Phe
 290 295 300

 atg tac gac cct aag aaa agg gcg acg gcc ggg gac tgc ctg gag agc 1080
 Met Tyr Asp Pro Lys Lys Arg Ala Thr Ala Gly Asp Cys Leu Glu Ser
 305 310 315 320

 tcc tat ttc aag gag aag ccc cta ccc tgt gag ccg gag ctc atg ccg 1128
 Ser Tyr Phe Lys Glu Lys Pro Leu Pro Cys Glu Pro Glu Leu Met Pro
 325 330 335

 acc ttt ccc cac cac cgc aac aag cgg gcc cca gcc acc tcc gag 1176
 Thr Phe Pro His His Arg Asn Lys Arg Ala Ala Pro Ala Thr Ser Glu
 340 345 350

 ggc cag agc aag cgc tgt aaa ccc tga cgggtggcct ggcacacgc 1223
 Gly Gln Ser Lys Arg Cys Lys Pro *
 355 360

 tgtattccca caccaggct tccgatcagt ggtgtctgtg aagggtgccg cgagccaggg 1283
 tgaccaggcg cccgggatcc agctcatccc cttggctggg aacatcctcc actgacttcc 1343
 tccccactgtc tgccctgaac ccactgctgc ccccagaaaa aggccgggtg acaccgggg 1403
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 ctcatgttgtt cctccctcgct atgttgaaa tgtgcaacca ctgcttcttg ggaggagttg 1523

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gctggatccc tgctccccac acggaggacc caacaggagg ccgtggctct gatgctgagc 1823
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20 25 30
Cys Arg Ser Val Lys Glu Phe Glu Lys Leu Asn Arg Ile Gly Glu Gly
35 40 45
Thr Tyr Gly Ile Val Tyr Arg Ala Arg Asp Thr Gln Thr Asp Glu Ile
50 55 60
Val Ala Leu Lys Lys Val Arg Met Asp Lys Glu Lys Asp Gly Ile Pro
65 70 75 80
Ile Ser Ser Leu Arg Glu Ile Thr Leu Leu Leu Arg Leu Arg His Pro
85 90 95
Asn Ile Val Glu Leu Lys Glu Val Val Val Gly Asn His Leu Glu Ser
100 105 110
Ile Phe Leu Val Met Gly Tyr Cys Glu Gln Asp Leu Ala Ser Leu Leu
115 120 125
Glu Asn Met Pro Thr Pro Phe Ser Glu Ala Gln Val Lys Cys Ile Val
130 135 140
Leu Gln Val Leu Arg Gly Leu Gln Tyr Leu His Arg Asn Phe Ile Ile
145 150 155 160
His Arg Asp Leu Lys Val Ser Asn Leu Leu Met Thr Asp Lys Gly Cys
165 170 175
Val Lys Thr Ala Asp Phe Gly Leu Ala Arg Ala Tyr Gly Val Pro Val
180 185 190
Lys Pro Met Thr Pro Lys Val Val Thr Leu Trp Tyr Arg Ala Pro Glu
195 200 205
Leu Leu Leu Gly Thr Thr Gln Thr Thr Ser Ile Asp Met Trp Ala
210 215 220
Val Gly Cys Ile Leu Ala Glu Leu Leu Ala His Arg Pro Leu Leu Pro
225 230 235 240
Gly Thr Ser Glu Ile His Gln Ile Asp Leu Ile Val Gln Leu Leu Gly
245 250 255
Thr Pro Ser Glu Asn Ile Trp Pro Gly Phe Ser Lys Leu Pro Leu Val
260 265 270
Gly Gln Tyr Ser Leu Arg Lys Gln Pro Tyr Asn Asn Leu Lys His Lys
275 280 285
Phe Pro Trp Leu Ser Glu Ala Gly Leu Arg Leu Leu His Phe Leu Phe
290 295 300
Met Tyr Asp Pro Lys Lys Arg Ala Thr Ala Gly Asp Cys Leu Glu Ser
305 310 315 320
Ser Tyr Phe Lys Glu Lys Pro Leu Pro Cys Glu Pro Glu Leu Met Pro
325 330 335
Thr Phe Pro His His Arg Asn Lys Arg Ala Ala Pro Ala Thr Ser Glu

340 Gly Gln Ser Lys Arg Cys Lys Pro 355	345 360	350
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ctttggccac tgggagggaaa a atg gcc agt gat acc cca ggt ttc tac atg 171		
Met Ala Ser Asp Thr Pro Gly Phe Tyr Met		
1	5	10
gac aaa ctt aat aaa tac cgc cag atg cac gga gta gcc att acg tat 219		
Asp Lys Leu Asn Lys Tyr Arg Gln Met His Gly Val Ala Ile Thr Tyr		
15	20	25
aaa gaa ctt agt act tcg gga cct cca cat gac aga agg ttt aca ttt 267		
Lys Glu Leu Ser Thr Ser Gly Pro Pro His Asp Arg Arg Phe Thr Phe		
30	35	40
caa gtt tta ata gat gag aag gaa ttt gga gaa gcc aaa ggt aga tca 315		
Gln Val Leu Ile Asp Glu Lys Glu Phe Gly Glu Ala Lys Gly Arg Ser		
45	50	55
aag acg gag gca aga aac gct gca gcc aaa tta gct gtt gat ata ctt 363		
Lys Thr Glu Ala Arg Asn Ala Ala Lys Leu Ala Val Asp Ile Leu		
60	65	70
gat aac gaa aac aag gtg gat tgt cac acg agt gca tgt gag caa ggc 411		
Asp Asn Glu Asn Lys Val Asp Cys His Thr Ser Ala Cys Glu Gln Gly		
75	80	85
90		
ttg ttc gtt ggt aac tac ata ggc ctt gtc aat agc ttt gcc cag aag 459		
Leu Phe Val Gly Asn Tyr Ile Gly Leu Val Asn Ser Phe Ala Gln Lys		
95	100	105
aaa aag ctg tct gta aat tat gaa cag tgt gag ccc aac tct gag ttg 507		
Lys Lys Leu Ser Val Asn Tyr Glu Gln Cys Glu Pro Asn Ser Glu Leu		
110	115	120
cct caa aga ttt att tgt aaa tgc aaa att ggg cag aca atg tat ggt 555		
Pro Gln Arg Phe Ile Cys Lys Cys Lys Ile Gly Gln Thr Met Tyr Gly		
125	130	135
act ggt tca ggt gtc acc aaa cag gag gca aag cag ttg gct gcg aaa 603		
Thr Gly Ser Gly Val Thr Lys Gln Glu Ala Lys Gln Leu Ala Ala Lys		
140	145	150

gaa gcc tat cag aag ctg tta aag agc ccg ccg aaa act gcc gga aca Glu Ala Tyr Gln Lys Leu Leu Lys Ser Pro Pro Lys Thr Ala Gly Thr 155	160	165	170	651
tcc tct agc gtt gtc aca tct aca ttc agt ggc ttt tcc agc agc tcg Ser Ser Ser Val Val Thr Ser Thr Phe Ser Gly Phe Ser Ser Ser Ser 175	180		185	699
tct atg aca agt aat ggt gtt tcc cag tca gca cct gga agt ttt tcc Ser Met Thr Ser Asn Gly Val Ser Gln Ser Ala Pro Gly Ser Phe Ser 190	195	200		747
tca gag aac gtg ttt acg aac ggt ctc gga gaa aat aaa agg aaa tca Ser Glu Asn Val Phe Thr Asn Gly Leu Gly Glu Asn Lys Arg Lys Ser 205	210	215		795
gga gta aaa gta tcc cct gat gat gtg caa aga aat aaa tat acc ttg Gly Val Lys Val Ser Pro Asp Asp Val Gln Arg Asn Lys Tyr Thr Leu 220	225	230		843
gac gcc agg ttt aac agc gat ttt gaa gac ata gaa gaa att ggc tta Asp Ala Arg Phe Asn Ser Asp Phe Glu Asp Ile Glu Glu Ile Gly Leu 235	240	245	250	891
ggt gga ttt ggt caa gtt ttc aaa gcg aaa cac aga att gat gga aag Gly Gly Phe Gly Gln Val Phe Lys Ala Lys His Arg Ile Asp Gly Lys 255	260	265		939
aga tac gct att aag cgc gtt aaa tat aac acg gag aag gcg gag cac Arg Tyr Ala Ile Lys Arg Val Lys Tyr Asn Thr Glu Lys Ala Glu His 270	275	280		987
gaa gta caa gcg ctg gca gaa ctc aat cac gtc aac att gtc caa tac Glu Val Gln Ala Leu Ala Glu Leu Asn His Val Asn Ile Val Gln Tyr 285	290	295		1035
cat agt tgt tgg gag gga gtt gac tat gat cct gag cac agc atg agt His Ser Cys Trp Glu Gly Val Asp Tyr Asp Pro Glu His Ser Met Ser 300	305	310		1083
gat aca agt cga tac aaa acc cgg tgc ctc ttt att caa atg gaa ttc Asp Thr Ser Arg Tyr Lys Thr Arg Cys Leu Phe Ile Gln Met Glu Phe 315	320	325	330	1131
tgt gat aaa gga act ttg gag caa tgg atg aga aac aga aat cag agt Cys Asp Lys Gly Thr Leu Glu Gln Trp Met Arg Asn Arg Asn Gln Ser 335	340	345		1179
aaa gtg gac aaa gct ttg att ttg gac tta tat gaa caa atc gtg acc Lys Val Asp Lys Ala Leu Ile Leu Asp Leu Tyr Glu Gln Ile Val Thr 350	355	360		1227
gga gtg gag tat ata cac tcg aaa ggg tta att cac aga gat ctt aag Gly Val Glu Tyr Ile His Ser Lys Gly Leu Ile His Arg Asp Leu Lys 365	370	375		1275
cca ggt aat ata ttt tta gta gat gaa aga cac att aag atc gga gac				1323

Pro Gly Asn Ile Phe Leu Val Asp Glu Arg His Ile Lys Ile Gly Asp				
380	385	390		
ttt ggc ctt gca aca gcc ctg gaa aat gat gga aaa tcc cga aca agg				1371
Phe Gly Leu Ala Thr Ala Leu Glu Asn Asp Gly Lys Ser Arg Thr Arg				
395	400	405		410
aga aca gga act ctt caa tac atg agt cca gaa cag tta ttt tta aag				1419
Arg Thr Gly Thr Leu Gln Tyr Met Ser Pro Glu Gln Leu Phe Leu Lys				
415	420	425		
cac tat gga aaa gaa gtg gac atc ttt gct ttg ggc ctt att cta gct				1467
His Tyr Gly Lys Glu Val Asp Ile Phe Ala Leu Gly Leu Ile Leu Ala				
430	435	440		
gaa ctt ctt cac acg tgc ttc acg gag tca gag aaa ata aag ttt ttc				1515
Glu Leu Leu His Thr Cys Phe Thr Glu Ser Glu Lys Ile Lys Phe Phe				
445	450	455		
gaa agt cta aga aaa ggc gac ttc tct aat gat ata ttc gac aac aaa				1563
Glu Ser Leu Arg Lys Gly Asp Phe Ser Asn Asp Ile Phe Asp Asn Lys				
460	465	470		
gaa aaa agc ctt cta aaa aaa cta ctc tca gag aaa ccc aag gac cga				1611
Glu Lys Ser Leu Leu Lys Lys Leu Ser Glu Lys Pro Lys Asp Arg				
475	480	485		490
cct gag aca tct gaa atc ctg aag acc ttg gct gaa tgg agg aac atc				1659
Pro Glu Thr Ser Glu Ile Leu Lys Thr Leu Ala Glu Trp Arg Asn Ile				
495	500	505		
tca gag aaa gaa aag aaa cac atg tta ggg cct ttc tga gaaaacattc				1708
Ser Glu Lys Glu Lys His Met Leu Gly Pro Phe *				
510	515			
cttctgccgt ggtttccctt taacgatctg cagtctgagg ggagtatcag tgaatattat				1768
ccttttttc ttaataccac tctcccagac agtttttgt tagggtgacc cacagacatt				1828
gtatttatta ggctatggaa aagtatgccc atttcctcaa ttgttaattt ctgggcctgt				1888
ggctggctag ctagccaat atgtaaatgc ttgtttctcg tctgccccaa gagaaaggca				1948
ggctccitgtg tggttggactca cagagccccaa aaagccaaact ggatgaggaa ggactctggc				2008
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acagacagac agacagagac acaaagacat ggactagaat ggaggaggaa gggaggaaagg				2128
gagggaggaa gagagagaga gagaaagaaa gagagagaga ggacatggag acaaaaatggc				2188
ttaagtttagc tggctcacct gagagactgt cccagaaaaac aggccaaacaa ctttccttat				2248
qctatataqa tqctcaqtq tctttatcat taaacaccaa qcqqqagtqc t				2299

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<211> 518

<212> PRT

<213> Mus musculus

<400> 24

Met Ala Ser Asp Thr Pro Gly Phe Tyr Met Asp Lys Leu Asn Lys Tyr

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Arg Gln Met His Gly Val Ala Ile Thr Tyr Lys Glu Leu Ser Thr Ser

20 25 30

Gly Pro Pro His Asp Arg Arg Phe Thr Phe Gln Val Leu Ile Asp Glu

35	40	45
Lys Glu Phe Gly Glu Ala Lys Gly Arg Ser Lys Thr Glu Ala Arg Asn		
50	55	60
Ala Ala Ala Lys Leu Ala Val Asp Ile Leu Asp Asn Glu Asn Lys Val		
65	70	75
Asp Cys His Thr Ser Ala Cys Glu Gln Gly Leu Phe Val Gly Asn Tyr		
85	90	95
Ile Gly Leu Val Asn Ser Phe Ala Gln Lys Lys Lys Leu Ser Val Asn		
100	105	110
Tyr Glu Gln Cys Glu Pro Asn Ser Glu Leu Pro Gln Arg Phe Ile Cys		
115	120	125
Lys Cys Lys Ile Gly Gln Thr Met Tyr Gly Thr Gly Ser Gly Val Thr		
130	135	140
Lys Gln Glu Ala Lys Gln Leu Ala Ala Lys Glu Ala Tyr Gln Lys Leu		
145	150	155
Leu Lys Ser Pro Pro Lys Thr Ala Gly Thr Ser Ser Ser Val Val Thr		
165	170	175
Ser Thr Phe Ser Gly Phe Ser Ser Ser Ser Met Thr Ser Asn Gly		
180	185	190
Val Ser Gln Ser Ala Pro Gly Ser Phe Ser Ser Glu Asn Val Phe Thr		
195	200	205
Asn Gly Leu Gly Glu Asn Lys Arg Lys Ser Gly Val Lys Val Ser Pro		
210	215	220
Asp Asp Val Gln Arg Asn Lys Tyr Thr Leu Asp Ala Arg Phe Asn Ser		
225	230	235
Asp Phe Glu Asp Ile Glu Glu Ile Gly Leu Gly Gly Phe Gly Gln Val		
245	250	255
Phe Lys Ala Lys His Arg Ile Asp Gly Lys Arg Tyr Ala Ile Lys Arg		
260	265	270
Val Lys Tyr Asn Thr Glu Lys Ala Glu His Glu Val Gln Ala Leu Ala		
275	280	285
Glu Leu Asn His Val Asn Ile Val Gln Tyr His Ser Cys Trp Glu Gly		
290	295	300
Val Asp Tyr Asp Pro Glu His Ser Met Ser Asp Thr Ser Arg Tyr Lys		
305	310	315
Thr Arg Cys Leu Phe Ile Gln Met Glu Phe Cys Asp Lys Gly Thr Leu		
325	330	335
Glu Gln Trp Met Arg Asn Arg Asn Gln Ser Lys Val Asp Lys Ala Leu		
340	345	350
Ile Leu Asp Leu Tyr Glu Gln Ile Val Thr Gly Val Glu Tyr Ile His		
355	360	365
Ser Lys Gly Leu Ile His Arg Asp Leu Lys Pro Gly Asn Ile Phe Leu		
370	375	380
Val Asp Glu Arg His Ile Lys Ile Gly Asp Phe Gly Leu Ala Thr Ala		
385	390	395
Leu Glu Asn Asp Gly Lys Ser Arg Thr Arg Arg Thr Gly Thr Leu Gln		
405	410	415
Tyr Met Ser Pro Glu Gln Leu Phe Leu Lys His Tyr Gly Lys Glu Val		
420	425	430
Asp Ile Phe Ala Leu Gly Leu Ile Leu Ala Glu Leu Leu His Thr Cys		
435	440	445
Phe Thr Glu Ser Glu Lys Ile Lys Phe Phe Glu Ser Leu Arg Lys Gly		
450	455	460
Asp Phe Ser Asn Asp Ile Phe Asp Asn Lys Glu Lys Ser Leu Leu Lys		
465	470	475
Lys Leu Leu Ser Glu Lys Pro Lys Asp Arg Pro Glu Thr Ser Glu Ile		
485	490	495

Leu Lys Thr Leu Ala Glu Trp Arg Asn Ile Ser Glu Lys Glu Lys Lys
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 His Met Leu Gly Pro Phe
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 taactaccc tcgtttcccta gatttcctt cattctgctc aagtcttcgc ctgtgtccga 120
 tccctatcta ctttctctcc tcttgtagca agcctcagac tccaggctt agcttaggtt 180
 tggttttctc ctggtgagaa ttcaagacc atg tct acg gaa ctc ttc tca tcc 234
 Met Ser Thr Glu Leu Phe Ser Ser
 1 5

aca aga gag gaa gga agc tct ggc tca gga ccc agt ttt agg tct aat 282
 Thr Arg Glu Glu Gly Ser Ser Gly Ser Gly Pro Ser Phe Arg Ser Asn
 10 15 20

caa agg aaa atg tta aac ctg ctc ctg gag aga gac act tcc ttt acc 330
 Gln Arg Lys Met Leu Asn Leu Leu Glu Arg Asp Thr Ser Phe Thr
 25 30 35 40

gtc tgt cca gat gtc cct aga act cca gtg ggc aaa ttt ctt ggt gat 378
 Val Cys Pro Asp Val Pro Arg Thr Pro Val Gly Lys Phe Leu Gly Asp
 45 50 55

tct gca aac cta agc att ttg tct gga gga acc cca aaa tgt tgc ctc 426
 Ser Ala Asn Leu Ser Ile Leu Ser Gly Gly Thr Pro Lys Cys Cys Leu
 60 65 70

gat ctt tcg aat ctt agc agt ggg gag ata act gcc act cag ctt acc 474
 Asp Leu Ser Asn Leu Ser Ser Gly Glu Ile Thr Ala Thr Gln Leu Thr
 75 80 85

act tct gca gac ctt gat gaa act ggt cac ctg gat tct tca gga ctt 522
 Thr Ser Ala Asp Leu Asp Glu Thr Gly His Leu Asp Ser Ser Gly Leu
 90 95 100

cag gaa gtg cat tta gct ggg atg aat cat gac cag cac cta atg aaa 570
 Gln Glu Val His Leu Ala Gly Met Asn His Asp Gln His Leu Met Lys
 105 110 115 120

tgt agc cca gca cag ctt ctt tgt agc act ccg aat ggt ttg gac cgt 618
 Cys Ser Pro Ala Gln Leu Leu Cys Ser Thr Pro Asn Gly Leu Asp Arg
 125 130 135

ggc cat aga aag aga gat gca atg tgt agt tca tct gca aat aaa gaa 666
 Gly His Arg Lys Arg Asp Ala Met Cys Ser Ser Ala Asn Lys Glu

140	145	150	
aat gac aat gga aac ttg gtg gac agt gaa atg aaa tat ttg ggc agt Asn Asp Asn Gly Asn Leu Val Asp Ser Glu Met Lys Tyr Leu Gly Ser 155	160	165	714
ccc att act act gtt cca aaa ttg gat aaa aat cca aac cta gga gaa Pro Ile Thr Thr Val Pro Lys Leu Asp Lys Asn Pro Asn Leu Gly Glu 170 175 180			762
gac cag gca gaa gag att tca gat gaa tta atg gag ttt tcc ctg aaa Asp Gln Ala Glu Glu Ile Ser Asp Glu Leu Met Glu Phe Ser Leu Lys 185 190 195 200			810
gat caa gaa gca aag gtg agc aga agt ggc cta tat cgc tcc ccg tcg Asp Gln Glu Ala Lys Val Ser Arg Ser Gly Leu Tyr Arg Ser Pro Ser 205 210 215			858
atg cca gag aac ttg aac agg cca aga ctg aag cag gtg gaa aaa ttc Met Pro Glu Asn Leu Asn Arg Pro Arg Leu Lys Gln Val Glu Lys Phe 220 225 230			906
aag gac aac aca ata cca gat aaa gtt aaa aag tat ttt tct ggc Lys Asp Asn Thr Ile Pro Asp Lys Val Lys Lys Tyr Phe Ser Gly 235 240 245			954
caa gga aag ctc agg aag ggc tta tgt tta aag aag aca gtc tct ctg Gln Gly Lys Leu Arg Lys Gly Leu Cys Leu Lys Lys Thr Val Ser Leu 250 255 260			1002
tgt gac att act atc act cag atg ctg gag gaa gat tct aac cag ggg Cys Asp Ile Thr Ile Thr Gln Met Leu Glu Glu Asp Ser Asn Gln Gly 265 270 275 280			1050
cac ctg att ggt gat ttt tcc aag gta tgt gcg ctg cca acc gtg tca His Leu Ile Gly Asp Phe Ser Lys Val Cys Ala Leu Pro Thr Val Ser 285 290 295			1098
ggg aaa cac caa gat ctg aag tat gtc aac cca gaa aca gtg gct gcc Gly Lys His Gln Asp Leu Lys Tyr Val Asn Pro Glu Thr Val Ala Ala 300 305 310			1146
tta ctg tcg ggg aag ttc cag ggt ctg att gag aag ttt tat gtc att Leu Leu Ser Gly Lys Phe Gln Gly Leu Glu Lys Phe Tyr Val Ile 315 320 325			1194
gat tgt cgc tat cca tat gag tat ctg gga gga cac atc cag gga gcc Asp Cys Arg Tyr Pro Tyr Glu Tyr Leu Gly Gly His Ile Gln Gly Ala 330 335 340			1242
tta aac tta tat agt cag gaa gaa ctg ttt aac ttc ttt ctg aag aag Leu Asn Leu Tyr Ser Gln Glu Glu Leu Phe Asn Phe Phe Leu Lys Lys 345 350 355 360			1290
ccc atc gtc cct ttg gac acc cag aag aga ata atc atc gtg ttc cac Pro Ile Val Pro Leu Asp Thr Gln Lys Arg Ile Ile Ile Val Phe His 365 370 375			1338

tgt gaa ttc tcc tca gag agg ggc ccc cga atg tgc cgc tgt ctg cgt		1386	
Cys Glu Phe Ser Ser Glu Arg Gly Pro Arg Met Cys Arg Cys Leu Arg			
380	385	390	
gaa gag gac agg tct ctg aac cag tat cct gca ttg tac tac cca gag		1434	
Glu Glu Asp Arg Ser Leu Asn Gln Tyr Pro Ala Leu Tyr Tyr Pro Glu			
395	400	405	
cta tat atc ctt aaa ggc ggc tac aga gac ttc ttt cca gaa tat atg		1482	
Leu Tyr Ile Leu Lys Gly Gly Tyr Arg Asp Phe Phe Pro Glu Tyr Met			
410	415	420	
gaa ctg tgt gaa cca cag agc tac tgc cct atg cat cat cag gac cac		1530	
Glu Leu Cys Glu Pro Gln Ser Tyr Cys Pro Met His His Gln Asp His			
425	430	435	440
aag act gag ttg ctg agg tgt cga agc cag agc aaa gtg cag gaa ggg		1578	
Lys Thr Glu Leu Leu Arg Cys Arg Ser Gln Ser Lys Val Gln Glu Gly			
445	450	455	
gag cgg cag ctg cgg gag cag att gcc ctt ctg gtg aag gac atg agc		1626	
Glu Arg Gln Leu Arg Glu Gln Ile Ala Leu Leu Val Lys Asp Met Ser			
460	465	470	
cca tga taacattcca gccactggct gctaacaagt cacaaaaaag acactgcaga		1682	
Pro *			
aaccctgagc agaaaagaggc cttctggatg gccaaaccca agattattaa aagatgtctc		1742	
tgcaaaccaa caggctacca acttgtatcc aggcctggga atggattagg tttcagcaga		1802	
gctgaaagct ggtggcagag tcctggagct ggctctataa ggcagccttg agttgcata		1862	
agatttgtat tggttcaggg aactctggca tccctttcc caactcctca tgtcttctca		1922	
caagccagcc aactctttct ctctgggctt cgggctatgc aagagcgttg tctaccttct		1982	
ttctttgtat ttcccttctt tgtttcccccc tctttctttt ttaaaaatgg aaaaataaac		2042	
actacagaat gag		2055	
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<213> Homo sapiens			
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Ser Gly Pro Ser Phe Arg Ser Asn Gln Arg Lys Met Leu Asn Leu Leu			
20 25 30			
Leu Glu Arg Asp Thr Ser Phe Thr Val Cys Pro Asp Val Pro Arg Thr			
35 40 45			
Pro Val Gly Lys Phe Leu Gly Asp Ser Ala Asn Leu Ser Ile Leu Ser			
50 55 60			
Gly Gly Thr Pro Lys Cys Cys Leu Asp Leu Ser Asn Leu Ser Ser Gly			
65 70 75 80			
Glu Ile Thr Ala Thr Gln Leu Thr Ser Ala Asp Leu Asp Glu Thr			
85 90 95			
Gly His Leu Asp Ser Ser Gly Leu Gln Glu Val His Leu Ala Gly Met			
100 105 110			

Asn His Asp Gln His Leu Met Lys Cys Ser Pro Ala Gln Leu Leu Cys
 115 120 125
 Ser Thr Pro Asn Gly Leu Asp Arg Gly His Arg Lys Arg Asp Ala Met
 130 135 140
 Cys Ser Ser Ser Ala Asn Lys Glu Asn Asp Asn Gly Asn Leu Val Asp
 145 150 155 160
 Ser Glu Met Lys Tyr Leu Gly Ser Pro Ile Thr Thr Val Pro Lys Leu
 165 170 175
 Asp Lys Asn Pro Asn Leu Gly Glu Asp Gln Ala Glu Glu Ile Ser Asp
 180 185 190
 Glu Leu Met Glu Phe Ser Leu Lys Asp Gln Glu Ala Lys Val Ser Arg
 195 200 205
 Ser Gly Leu Tyr Arg Ser Pro Ser Met Pro Glu Asn Leu Asn Arg Pro
 210 215 220
 Arg Leu Lys Gln Val Glu Lys Phe Lys Asp Asn Thr Ile Pro Asp Lys
 225 230 235 240
 Val Lys Lys Tyr Phe Ser Gly Gln Gly Lys Leu Arg Lys Gly Leu
 245 250 255
 Cys Leu Lys Lys Thr Val Ser Leu Cys Asp Ile Thr Ile Thr Gln Met
 260 265 270
 Leu Glu Glu Asp Ser Asn Gln Gly His Leu Ile Gly Asp Phe Ser Lys
 275 280 285
 Val Cys Ala Leu Pro Thr Val Ser Gly Lys His Gln Asp Leu Lys Tyr
 290 295 300
 Val Asn Pro Glu Thr Val Ala Ala Leu Leu Ser Gly Lys Phe Gln Gly
 305 310 315 320
 Leu Ile Glu Lys Phe Tyr Val Ile Asp Cys Arg Tyr Pro Tyr Glu Tyr
 325 330 335
 Leu Gly Gly His Ile Gln Gly Ala Leu Asn Leu Tyr Ser Gln Glu Glu
 340 345 350
 Leu Phe Asn Phe Phe Leu Lys Lys Pro Ile Val Pro Leu Asp Thr Gln
 355 360 365
 Lys Arg Ile Ile Ile Val Phe His Cys Glu Phe Ser Ser Glu Arg Gly
 370 375 380
 Pro Arg Met Cys Arg Cys Leu Arg Glu Glu Asp Arg Ser Leu Asn Gln
 385 390 395 400
 Tyr Pro Ala Leu Tyr Tyr Pro Glu Leu Tyr Ile Leu Lys Gly Gly Tyr
 405 410 415
 Arg Asp Phe Phe Pro Glu Tyr Met Glu Leu Cys Glu Pro Gln Ser Tyr
 420 425 430
 Cys Pro Met His His Gln Asp His Lys Thr Glu Leu Leu Arg Cys Arg
 435 440 445
 Ser Gln Ser Lys Val Gln Glu Gly Glu Arg Gln Leu Arg Glu Gln Ile
 450 455 460
 Ala Leu Leu Val Lys Asp Met Ser Pro
 465 470

<210> 27
 <211> 17
 <212> PRT
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<400> 27
 Ser Gly Leu Tyr Arg Ser Pro Ser Met Pro Glu Asn Leu Asn Arg Pro
 1 5 10 15
 Arg

<210> 28
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 28
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 1 5 10

<210> 29
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 <213> Saccharomyces cerevisiae

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Met Ser Thr Asn Ser Phe His Asp Tyr Val Asp Leu Lys Ser Arg Thr						
1 5 10 15						
aat aca cga cag ttt tca gat gac gaa gag ttc act acg cct cca aaa						96
Asn Thr Arg Gln Phe Ser Asp Asp Glu Glu Phe Thr Thr Pro Pro Lys						
20 25 30						
cta agc aat ttc gga tca gct tta ctt tcc cac aca gaa aaa act tca						144
Leu Ser Asn Phe Gly Ser Ala Leu Leu Ser His Thr Glu Lys Thr Ser						
35 40 45						
gca tca gag ata tta tca agt cat aat aat gac aag atc gca aat cga						192
Ala Ser Glu Ile Leu Ser Ser His Asn Asn Asp Lys Ile Ala Asn Arg						
50 55 60						
tta gaa gaa atg gac agg agt tca tca agg agt cac ccc cca ccg tca						240
Leu Glu Glu Met Asp Arg Ser Ser Ser Arg Ser His Pro Pro Pro Ser						
65 70 75 80						
atg ggc aat ttg aca tcc ggt cat act agt acc tca tcg cat tca acc						288
Met Gly Asn Leu Thr Ser Gly His Thr Ser Ser His Ser Thr						
85 90 95						
ttg ttc gga cga tat ctg aga aat aat cac cag act agc atg acg acg						336
Leu Phe Gly Arg Tyr Leu Arg Asn Asn His Gln Thr Ser Met Thr Thr						
100 105 110						
atg aac act agt gac ata gag ata aat gtt gga aat agt ctt gat aag						384
Met Asn Thr Ser Asp Ile Glu Ile Asn Val Gly Asn Ser Leu Asp Lys						
115 120 125						
agt ttt gaa agg ata agg aat ttg cga caa aat atg aaa gaa gat att						432
Ser Phe Glu Arg Ile Arg Asn Leu Arg Gln Asn Met Lys Glu Asp Ile						

130	135	140	
acg gca aag tat gct gaa agg aga agt aag aga ttt tta ata tcc aat Thr Ala Lys Tyr Ala Glu Arg Arg Ser Lys Arg Phe Leu Ile Ser Asn	150	155	480
145			160
agg aca acg aag ctg ggt cct gca aag aga gcg atg act ttg aca aat Arg Thr Thr Lys Leu Gly Pro Ala Lys Arg Ala Met Thr Leu Thr Asn			528
165	170		175
atc ttt gat gag gat gtg cct aac tct cca aac cag cca ata aat gca Ile Phe Asp Glu Asp Val Pro Asn Ser Pro Asn Gln Pro Ile Asn Ala	180	185	576
180		190	
agg gag aca gtg gaa tta cca ctt gag gat tct cac caa aca aac ttt Arg Glu Thr Val Glu Leu Pro Leu Glu Asp Ser His Gln Thr Asn Phe	195	200	624
195		205	
aaa gaa cga aga gag aat acg gat tat gat tca att gat ttt gga gat Lys Glu Arg Arg Glu Asn Thr Asp Tyr Asp Ser Ile Asp Phe Gly Asp	210	215	672
210		220	
ttg aat cct atc cag tat att aaa aaa cat aat ctt ccc aca agt gac Leu Asn Pro Ile Gln Tyr Ile Lys Lys His Asn Leu Pro Thr Ser Asp	225	230	720
225		235	240
ctt cca cta ata tct caa atc tac ttt gat aaa caa aga gaa gaa aat Leu Pro Leu Ile Ser Gln Ile Tyr Phe Asp Lys Gln Arg Glu Glu Asn	245	250	768
245		255	
aga caa gca gca ctc cga aaa cat agt tcc aga gaa ttg ctt tat aaa Arg Gln Ala Ala Leu Arg Lys His Ser Ser Arg Glu Leu Leu Tyr Lys	260	265	816
260		270	
agt agg tct tct tcc tct tca ctt tct agt aac aac tta ttg gca aac Ser Arg Ser Ser Ser Ser Leu Ser Ser Asn Asn Leu Leu Ala Asn	275	280	864
275		285	
aag gac aat tct ata aca tcc aat aat ggt tct caa ccc agg cga aaa Lys Asp Asn Ser Ile Thr Ser Asn Asn Gly Ser Gln Pro Arg Arg Lys	290	295	912
290		300	
gtt tct act gga tca tct tca tct aag tca tcg atc gaa ata aga aga Val Ser Thr Gly Ser Ser Ser Lys Ser Ser Ile Glu Ile Arg Arg	305	310	960
305		315	320
gct ctc aag gag aat att gat act agc aat aac agc aat ttc aac agc Ala Leu Lys Glu Asn Ile Asp Thr Ser Asn Asn Ser Asn Phe Asn Ser	325	330	1008
325		335	
cca att cat aaa att tat aaa gga att tcc aga aat aaa gat tcc gac Pro Ile His Lys Ile Tyr Lys Gly Ile Ser Arg Asn Lys Asp Ser Asp	340	345	1056
340		350	
tcc gaa aaa aga gaa gta ctg cga aac ata agc ata aat gca aat cac Ser Glu Lys Arg Glu Val Leu Arg Asn Ile Ser Ile Asn Ala Asn His	355	360	1104
355		365	

gct gat aat ctc ctt caa caa gag aat aag aga cta aaa cga tca ttg Ala Asp Asn Leu Leu Gln Gln Glu Asn Lys Arg Leu Lys Arg Ser Leu	370	375	380	1152
gat gat gca ata acg aat gag aat ata aac agt aaa aat cta gaa gta Asp Asp Ala Ile Thr Asn Glu Asn Ile Asn Ser Lys Asn Leu Glu Val	385	390	395	400
ttt tac cat cga cct gct ccc aaa cct cca gtc acc aag aaa gtt gaa Phe Tyr His Arg Pro Ala Pro Lys Pro Pro Val Thr Lys Lys Val Glu	405	410	415	1248
att gtt gaa cct gca aag tcc gct tct tta tcg aat aat aga aat ata Ile Val Glu Pro Ala Lys Ser Ala Ser Leu Ser Asn Asn Arg Asn Ile	420	425	430	1296
att aca gta aat gac tcc cag tac gaa aaa ata gaa ctt ttg ggt aga Ile Thr Val Asn Asp Ser Gln Tyr Glu Lys Ile Glu Leu Leu Gly Arg	435	440	445	1344
ggg gga tcc tcc aga gtt tac aag gtg aaa gga tct ggc aat agg gta Gly Gly Ser Ser Arg Val Tyr Lys Val Lys Gly Ser Gly Asn Arg Val	450	455	460	1392
tac gcg ctc aaa agg gtg tct ttt gac gct ttt gac gat tca agt att Tyr Ala Leu Lys Arg Val Ser Phe Asp Ala Phe Asp Asp Ser Ser Ile	465	470	475	1440
gat gga ttc aaa gga gaa ata gaa ctt ctg gaa aaa ttg aaa gac caa Asp Gly Phe Lys Gly Glu Ile Glu Leu Leu Glu Lys Leu Lys Asp Gln	485	490	495	1488
aag cgt gta atc caa cta cta gat tat gaa atg ggg gat ggt tta ttg Lys Arg Val Ile Gln Leu Leu Asp Tyr Glu Met Gly Asp Gly Leu Leu	500	505	510	1536
tat ttg ata atg gaa tgt ggt gat cat gat ttg tca caa atc ctt aac Tyr Leu Ile Met Glu Cys Gly Asp His Asp Leu Ser Gln Ile Leu Asn	515	520	525	1584
caa aga agc ggc atg cca ctg gat ttt aat ttt gtt aga ttc tat aca Gln Arg Ser Gly Met Pro Leu Asp Phe Asn Phe Val Arg Phe Tyr Thr	530	535	540	1632
aag gaa atg ttg ctg tgc att aaa gta gtt cat gat gcg ggc ata gtt Lys Glu Met Leu Leu Cys Ile Lys Val Val His Asp Ala Gly Ile Val	545	550	555	1680
cat tcg gat tta aaa cct gca aat ttt gtt tta gtg aaa ggt atc tta His Ser Asp Leu Lys Pro Ala Asn Phe Val Leu Val Lys Gly Ile Leu	565	570	575	1728
aaa atc att gat ttt ggt ata gca aac gcg gta ccg gaa cat acg gtg Lys Ile Ile Asp Phe Gly Ile Ala Asn Ala Val Pro Glu His Thr Val	580	585	590	1776

aat ata tat cgt gaa act caa att ggg act cca aat tat atg gca cca Asn Ile Tyr Arg Glu Thr Gln Ile Gly Thr Pro Asn Tyr Met Ala Pro	595	600	605	1824	
gaa gca cta gtt gct atg aat tac aca caa aat agt gag aac caa cat Glu Ala Leu Val Ala Met Asn Tyr Thr Gln Asn Ser Glu Asn Gln His	610	615	620	1872	
gag gga aac aag tgg aaa gtg ggg aga cca tct gat atg tgg tca tgc Glu Gly Asn Lys Trp Lys Val Gly Arg Pro Ser Asp Met Trp Ser Cys	625	630	635	1920	
ggt tgt att ata tat cag atg att tac ggg aaa ccc cca tat ggc agt Gly Cys Ile Ile Tyr Gln Met Ile Tyr Gly Lys Pro Pro Tyr Gly Ser	645	650	655	1968	
ttc caa ggc caa aat agg ctg ttg gct att atg aat cct gat gtg aaa Phe Gln Gly Gln Asn Arg Leu Leu Ala Ile Met Asn Pro Asp Val Lys	660	665	670	2016	
atc cca ttt cct gaa cat act agc aat aat gaa aag att cca aag tct Ile Pro Phe Pro Glu His Thr Ser Asn Asn Glu Lys Ile Pro Lys Ser	675	680	685	2064	
gcc att gaa tta atg aaa gca tgt ctg tac agg aac cca gac aaa aga Ala Ile Glu Leu Met Lys Ala Cys Leu Tyr Arg Asn Pro Asp Lys Arg	690	695	700	2112	
tgg act gtg gat aaa gtc ctg agt agc act ttc ctt caa cct ttt atg Trp Thr Val Asp Lys Val Leu Ser Ser Thr Phe Leu Gln Pro Phe Met	705	710	715	720	2160
ata tcc gga tcg att atg gaa gac ctt att agg aat gcc gtt aga tat Ile Ser Gly Ser Ile Met Glu Asp Leu Ile Arg Asn Ala Val Arg Tyr	725	730	735	2208	
ggc tct gag aag cct cat ata tca caa gat gat ctc aat gat gtg gta Gly Ser Glu Lys Pro His Ile Ser Gln Asp Asp Leu Asn Asp Val Val	740	745	750	2256	
gac act gtt tta agg aaa ttt gca gat tac aaa att tag Asp Thr Val Leu Arg Lys Phe Ala Asp Tyr Lys Ile *	755	760		2295	

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<212> PRT
<213> *Saccharomyces cerevisiae*

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Asn Thr Arg Gln Phe Ser Asp Asp Glu Glu Phe Thr Thr Pro Pro Lys
20 25 30
Leu Ser Asn Phe Gly Ser Ala Leu Leu Ser His Thr Glu Lys Thr Ser
35 40 45

Ala Ser Glu Ile Leu Ser Ser His Asn Asn Asp Lys Ile Ala Asn Arg
 50 55 60
 Leu Glu Glu Met Asp Arg Ser Ser Ser Arg Ser His Pro Pro Pro Ser
 65 70 75 80
 Met Gly Asn Leu Thr Ser Gly His Thr Ser Thr Ser Ser His Ser Thr
 85 90 95
 Leu Phe Gly Arg Tyr Leu Arg Asn Asn His Gln Thr Ser Met Thr Thr
 100 105 110
 Met Asn Thr Ser Asp Ile Glu Ile Asn Val Gly Asn Ser Leu Asp Lys
 115 120 125
 Ser Phe Glu Arg Ile Arg Asn Leu Arg Gln Asn Met Lys Glu Asp Ile
 130 135 140
 Thr Ala Lys Tyr Ala Glu Arg Arg Ser Lys Arg Phe Leu Ile Ser Asn
 145 150 155 160
 Arg Thr Thr Lys Leu Gly Pro Ala Lys Arg Ala Met Thr Leu Thr Asn
 165 170 175
 Ile Phe Asp Glu Asp Val Pro Asn Ser Pro Asn Gln Pro Ile Asn Ala
 180 185 190
 Arg Glu Thr Val Glu Leu Pro Leu Glu Asp Ser His Gln Thr Asn Phe
 195 200 205
 Lys Glu Arg Arg Glu Asn Thr Asp Tyr Asp Ser Ile Asp Phe Gly Asp
 210 215 220
 Leu Asn Pro Ile Gln Tyr Ile Lys Lys His Asn Leu Pro Thr Ser Asp
 225 230 235 240
 Leu Pro Leu Ile Ser Gln Ile Tyr Phe Asp Lys Gln Arg Glu Glu Asn
 245 250 255
 Arg Gln Ala Ala Leu Arg Lys His Ser Ser Arg Glu Leu Leu Tyr Lys
 260 265 270
 Ser Arg Ser Ser Ser Ser Leu Ser Ser Asn Asn Leu Leu Ala Asn
 275 280 285
 Lys Asp Asn Ser Ile Thr Ser Asn Asn Gly Ser Gln Pro Arg Arg Lys
 290 295 300
 Val Ser Thr Gly Ser Ser Ser Lys Ser Ser Ile Glu Ile Arg Arg
 305 310 315 320
 Ala Leu Lys Glu Asn Ile Asp Thr Ser Asn Asn Ser Asn Phe Asn Ser
 325 330 335
 Pro Ile His Lys Ile Tyr Lys Gly Ile Ser Arg Asn Lys Asp Ser Asp
 340 345 350
 Ser Glu Lys Arg Glu Val Leu Arg Asn Ile Ser Ile Asn Ala Asn His
 355 360 365
 Ala Asp Asn Leu Leu Gln Gln Glu Asn Lys Arg Leu Lys Arg Ser Leu
 370 375 380
 Asp Asp Ala Ile Thr Asn Glu Asn Ile Asn Ser Lys Asn Leu Glu Val
 385 390 395 400
 Phe Tyr His Arg Pro Ala Pro Lys Pro Pro Val Thr Lys Lys Val Glu
 405 410 415
 Ile Val Glu Pro Ala Lys Ser Ala Ser Leu Ser Asn Asn Arg Asn Ile
 420 425 430
 Ile Thr Val Asn Asp Ser Gln Tyr Glu Lys Ile Glu Leu Leu Gly Arg
 435 440 445
 Gly Gly Ser Ser Arg Val Tyr Lys Val Lys Gly Ser Gly Asn Arg Val
 450 455 460
 Tyr Ala Leu Lys Arg Val Ser Phe Asp Ala Phe Asp Asp Ser Ser Ile
 465 470 475 480
 Asp Gly Phe Lys Gly Glu Ile Glu Leu Leu Glu Lys Leu Lys Asp Gln
 485 490 495
 Lys Arg Val Ile Gln Leu Leu Asp Tyr Glu Met Gly Asp Gly Leu Leu

500	505	510
Tyr Leu Ile Met Glu Cys Gly Asp His Asp Leu Ser Gln Ile Leu Asn		
515	520	525
Gln Arg Ser Gly Met Pro Leu Asp Phe Asn Phe Val Arg Phe Tyr Thr		
530	535	540
Lys Glu Met Leu Leu Cys Ile Lys Val Val His Asp Ala Gly Ile Val		
545	550	555
His Ser Asp Leu Lys Pro Ala Asn Phe Val Leu Val Lys Gly Ile Leu		
565	570	575
Lys Ile Ile Asp Phe Gly Ile Ala Asn Ala Val Pro Glu His Thr Val		
580	585	590
Asn Ile Tyr Arg Glu Thr Gln Ile Gly Thr Pro Asn Tyr Met Ala Pro		
595	600	605
Glu Ala Leu Val Ala Met Asn Tyr Thr Gln Asn Ser Glu Asn Gln His		
610	615	620
Glu Gly Asn Lys Trp Lys Val Gly Arg Pro Ser Asp Met Trp Ser Cys		
625	630	635
Gly Cys Ile Ile Tyr Gln Met Ile Tyr Gly Lys Pro Pro Tyr Gly Ser		
645	650	655
Phe Gln Gly Gln Asn Arg Leu Leu Ala Ile Met Asn Pro Asp Val Lys		
660	665	670
Ile Pro Phe Pro Glu His Thr Ser Asn Asn Glu Lys Ile Pro Lys Ser		
675	680	685
Ala Ile Glu Leu Met Lys Ala Cys Leu Tyr Arg Asn Pro Asp Lys Arg		
690	695	700
Trp Thr Val Asp Lys Val Leu Ser Ser Thr Phe Leu Gln Pro Phe Met		
705	710	715
Ile Ser Gly Ser Ile Met Glu Asp Leu Ile Arg Asn Ala Val Arg Tyr		
725	730	735
Gly Ser Glu Lys Pro His Ile Ser Gln Asp Asp Leu Asn Asp Val Val		
740	745	750
Asp Thr Val Leu Arg Lys Phe Ala Asp Tyr Lys Ile		
755	760	

<210> 31
<211> 2079
<212> DNA
<213> Schizosaccharomyces pombe

<220>
<221> CDS
<222> (30) ... (2066)

<400> 31		
ggaatgctcg ttttttagta actgtgttt atg tct aag cgc aat cct cct gtg		53
Met Ser Lys Arg Asn Pro Pro Val		
1	5	
act aat atc gcg gac ttg qtg tca gat tct tcc tta gat gaa gac tcg		101
Thr Asn Ile Ala Asp Leu Val Ser Asp Ser Ser Leu Asp Glu Asp Ser		
10	15	20
ctt tct ttt ctc gaa gag ctt cag gat cca gaa tta tac ttc aaa aac		149
Leu Ser Phe Leu Glu Leu Gln Asp Pro Glu Leu Tyr Phe Lys Asn		
25	30	35
		40

gac act ttc tct tcc aag agt agc cat tct gat ggc acc gtt act ggg Asp Thr Phe Ser Ser Lys Ser Ser His Ser Asp Gly Thr Val Thr Gly	45	50	55	197
gat acg ttg cgt agg cag tca agc ggt gca act gct tta gag aga ttg Asp Thr Leu Arg Arg Gln Ser Ser Gly Ala Thr Ala Leu Glu Arg Leu	60	65	70	245
gtc tca cat cct cgt act aaa aat ttt gat ttg caa gga aat gga gga Val Ser His Pro Arg Thr Lys Asn Phe Asp Leu Gln Gly Asn Gly Gly	75	80	85	293
caa aat tct gct ttg aag gaa gtg aat act cca gca tat cag tca atg Gln Asn Ser Ala Leu Lys Glu Val Asn Thr Pro Ala Tyr Gln Ser Met	90	95	100	341
cac cat ttc gag cat tta ata aca ccc ttg ccc tct act aat gcg tct His His Phe Glu His Leu Ile Thr Pro Leu Pro Ser Thr Asn Ala Ser	105	110	115	389
cac agt gaa gtt tca ctc agt gca gga gtg aat gat ctc aat tct aat His Ser Glu Val Ser Leu Ser Ala Gly Val Asn Asp Leu Asn Ser Asn	125	130	135	437
tcg gag cat gat ttg tta cct aaa agt gta aac aaa acc ccc ggt tct Ser Glu His Asp Leu Leu Pro Lys Ser Val Asn Lys Thr Pro Gly Ser	140	145	150	485
tta tca att tca aga cga cga aga atc ggc aga att gga tta ggc cct Leu Ser Ile Ser Arg Arg Arg Ile Gly Arg Ile Gly Leu Gly Pro	155	160	165	533
cca aag cgt gct gag tac acg ttg acg gat ccc tcg aag act tcc gat Pro Lys Arg Ala Glu Tyr Thr Leu Thr Asp Pro Ser Lys Thr Ser Asp	170	175	180	581
acc aaa aac tct aca gaa gca gat gag gat att gaa atg aaa tct cga Thr Lys Asn Ser Thr Glu Ala Asp Glu Asp Ile Glu Met Lys Ser Arg	185	190	195	629
gaa gta tca cca gct tcc aac tct gtt gct gca aca act tta aaa cct Glu Val Ser Pro Ala Ser Asn Ser Val Ala Ala Thr Thr Leu Lys Pro	205	210	215	677
ctg cag ctg cat aac act cct ttg caa aca tcc cag gag cat ccc aaa Leu Gln Leu His Asn Thr Pro Leu Gln Thr Ser Gln Glu His Pro Lys	220	225	230	725
cct tct ttt cat cct tct cag ttt gag agc tct ttt tct cct agg gtg Pro Ser Phe His Pro Ser Gln Phe Glu Ser Ser Phe Ser Pro Arg Val	235	240	245	773
cag ttt gat cac gat gtt gaa aga aga gct agt gaa ctt cat tct cgt Gln Phe Asp His Asp Val Glu Arg Arg Ala Ser Glu Leu His Ser Arg	250	255	260	821
cca gtc acc gtt ttc caa gag cct cag cgt tct gct tct caa cca tat				869

Pro Val Thr Val Phe Gln Glu Pro Gln Arg Ser Ala Ser Gln Pro Tyr			
265	270	275	280
gaa tct cat gct ctt tct cca aag gtg gct ccg tta ttt gat aac agt			917
Glu Ser His Ala Leu Ser Pro Lys Val Ala Pro Leu Phe Asp Asn Ser			
285	290	295	
caa gct act ccc ata ccc aag cgt cag cag gac gtt gtt act gtt gcc			965
Gln Ala Thr Pro Ile Pro Lys Arg Gln Gln Asp Val Val Thr Val Ala			
300	305	310	
aat cta caa ttt atc aaa tta gga gtt gtt gga aag ggt gga agt agt			1013
Asn Leu Gln Phe Ile Lys Leu Gly Val Val Gly Lys Gly Ser Ser			
315	320	325	
atg gta tat cgc ata ttt tcc ccc gat aac agt cgt tta tac gct ttg			1061
Met Val Tyr Arg Ile Phe Ser Pro Asp Asn Ser Arg Leu Tyr Ala Leu			
330	335	340	
aaa gag gtg aac ttt att aat gca gac caa act act ata caa gga tac			1109
Lys Glu Val Asn Phe Ile Asn Ala Asp Gln Thr Thr Ile Gln Gly Tyr			
345	350	355	360
aag aac gaa att gca tta tta aga aag ctt tca ggc aat gat cgc ata			1157
Lys Asn Glu Ile Ala Leu Leu Arg Lys Leu Ser Gly Asn Asp Arg Ile			
365	370	375	
att aaa tta tat gct gcc gaa gtt aat gat act tta ggg caa ctc aat			1205
Ile Lys Leu Tyr Ala Ala Glu Val Asn Asp Thr Leu Gly Gln Leu Asn			
380	385	390	
atg gtg atg gaa tgc gga gaa acg gat tta gca aac ctt tta atg aaa			1253
Met Val Met Glu Cys Gly Glu Thr Asp Leu Ala Asn Leu Leu Met Lys			
395	400	405	
aac atg aag aaa ccc att aat ctt aat ttc atc aga atg tat tgg gag			1301
Asn Met Lys Lys Pro Ile Asn Leu Asn Phe Ile Arg Met Tyr Trp Glu			
410	415	420	
caa atg cta gag gcg gtc cag gta gtt cat gat caa aat ata gtg cat			1349
Gln Met Leu Glu Ala Val Gln Val Val His Asp Gln Asn Ile Val His			
425	430	435	440
tcg gat ttg aag ccg gcc aat ttc ctg ctt gta gaa ggg aat ttg aag			1397
Ser Asp Leu Lys Pro Ala Asn Phe Leu Leu Val Glu Gly Asn Leu Lys			
445	450	455	
ctg att gat ttt ggc att gcc aaa gca att ggt aat gac acc act aat			1445
Leu Ile Asp Phe Gly Ile Ala Lys Ala Ile Gly Asn Asp Thr Thr Asn			
460	465	470	
atc cat cgt gat tcc cac atc ggt act att aat tat atg gca cct gaa			1493
Ile His Arg Asp Ser His Ile Gly Thr Ile Asn Tyr Met Ala Pro Glu			
475	480	485	
gct ttg aca gac atg aat gct cac aca aac tct ggc gtg aaa ctc gta			1541
Ala Leu Thr Asp Met Asn Ala His Thr Asn Ser Gly Val Lys Leu Val			

490	495	500	
aag ttg ggc agg ccc agc gac gtg tgg agt ttg gga tgt ata tta tat Lys Leu Gly Arg Pro Ser Asp Val Trp Ser Leu Gly Cys Ile Leu Tyr 505	510	515	1589
cag atg gtg tat ggg agg gcc ccg ttt gct cat cta aaa atg atc caa Gln Met Val Tyr Gly Arg Ala Pro Phe Ala His Leu Lys Met Ile Gln 525	530	535	1637
gct ata gca gct atc cct aat gaa caa tat cac att cat ttc ccc gaa Ala Ile Ala Ala Ile Pro Asn Glu Gln Tyr His Ile His Phe Pro Glu 540	545	550	1685
gtt gcc tta cct gct aat gct gtc cag gag aaa gag gga tcg ttg cca Val Ala Leu Pro Ala Asn Ala Val Gln Glu Lys Glu Gly Ser Leu Pro 555	560	565	1733
ggg gta act gtc ggg cct gat cta atg gat gtt atg aaa aga tgc ctg Gly Val Thr Val Gly Pro Asp Leu Met Asp Val Met Lys Arg Cys Leu 570	575	580	1781
gaa agg gat caa cg ^g aag aga ctt aca ata ccg gaa ttg ctg gtt cat Glu Arg Asp Gln Arg Lys Arg Leu Thr Ile Pro Glu Leu Leu Val His 585	590	595	1829
ccc ttt tta aac cct ttg cca tcc tat ttg aca cct ttg gcc aaa aag Pro Phe Leu Asn Pro Leu Pro Ser Tyr Leu Thr Pro Leu Ala Lys Lys 605	610	615	1877
ccg tta cct gtt tct ggg cac acc aat aat gct cat cca ctt aga ctc Pro Leu Pro Val Ser Gly His Thr Asn Asn Ala His Pro Leu Arg Leu 620	625	630	1925
agc aca gaa atc tca gct tct caa tta tca atg att ata gaa agg tcg Ser Thr Glu Ile Ser Ala Ser Gln Leu Ser Met Ile Ile Glu Arg Ser 635	640	645	1973
gtg gag ttg agt aag cac aag cga tta aat aag gaa ctt att gat agc Val Glu Leu Ser Lys His Lys Arg Leu Asn Lys Glu Leu Ile Asp Ser 650	655	660	2021
atg gct tat gat tgc gtt agc aat tta cga aaa atg cca gaa tag Met Ala Tyr Asp Cys Val Ser Asn Leu Arg Lys Met Pro Glu *	670	675	2066
aggcactaaa ttt			2079
<210> 32			
<211> 678			
<212> PRT			
<213> Schizosaccharomyces pombe			
<400> 32			
Met Ser Lys Arg Asn Pro Pro Val Thr Asn Ile Ala Asp Leu Val Ser 1 5 10 15			
Asp Ser Ser Leu Asp Glu Asp Ser Leu Ser Phe Leu Glu Glu Leu Gln			

20	25	30
Asp Pro Glu Leu Tyr Phe Lys Asn Asp Thr Phe Ser Ser Lys Ser Ser		
35	40	45
His Ser Asp Gly Thr Val Thr Gly Asp Thr Leu Arg Arg Gln Ser Ser		
50	55	60
Gly Ala Thr Ala Leu Glu Arg Leu Val Ser His Pro Arg Thr Lys Asn		
65	70	75
Phe Asp Leu Gln Gly Asn Gly Gln Asn Ser Ala Leu Lys Glu Val		
85	90	95
Asn Thr Pro Ala Tyr Gln Ser Met His His Phe Glu His Leu Ile Thr		
100	105	110
Pro Leu Pro Ser Thr Asn Ala Ser His Ser Glu Val Ser Leu Ser Ala		
115	120	125
Gly Val Asn Asp Leu Asn Ser Asn Ser Glu His Asp Leu Leu Pro Lys		
130	135	140
Ser Val Asn Lys Thr Pro Gly Ser Leu Ser Ile Ser Arg Arg Arg Arg		
145	150	155
Ile Gly Arg Ile Gly Leu Gly Pro Pro Lys Arg Ala Glu Tyr Thr Leu		
165	170	175
Thr Asp Pro Ser Lys Thr Ser Asp Thr Lys Asn Ser Thr Glu Ala Asp		
180	185	190
Glu Asp Ile Glu Met Lys Ser Arg Glu Val Ser Pro Ala Ser Asn Ser		
195	200	205
Val Ala Ala Thr Thr Leu Lys Pro Leu Gln Leu His Asn Thr Pro Leu		
210	215	220
Gln Thr Ser Gln Glu His Pro Lys Pro Ser Phe His Pro Ser Gln Phe		
225	230	235
Glu Ser Ser Phe Ser Pro Arg Val Gln Phe Asp His Asp Val Glu Arg		
245	250	255
Arg Ala Ser Glu Leu His Ser Arg Pro Val Thr Val Phe Gln Glu Pro		
260	265	270
Gln Arg Ser Ala Ser Gln Pro Tyr Glu Ser His Ala Leu Ser Pro Lys		
275	280	285
Val Ala Pro Leu Phe Asp Asn Ser Gln Ala Thr Pro Ile Pro Lys Arg		
290	295	300
Gln Gln Asp Val Val Thr Val Ala Asn Leu Gln Phe Ile Lys Leu Gly		
305	310	315
Val Val Gly Lys Gly Ser Ser Met Val Tyr Arg Ile Phe Ser Pro		
325	330	335
Asp Asn Ser Arg Leu Tyr Ala Leu Lys Glu Val Asn Phe Ile Asn Ala		
340	345	350
Asp Gln Thr Thr Ile Gln Gly Tyr Lys Asn Glu Ile Ala Leu Leu Arg		
355	360	365
Lys Leu Ser Gly Asn Asp Arg Ile Ile Lys Leu Tyr Ala Ala Glu Val		
370	375	380
Asn Asp Thr Leu Gly Gln Leu Asn Met Val Met Glu Cys Gly Glu Thr		
385	390	395
Asp Leu Ala Asn Leu Leu Met Lys Asn Met Lys Lys Pro Ile Asn Leu		
405	410	415
Asn Phe Ile Arg Met Tyr Trp Glu Gln Met Leu Glu Ala Val Gln Val		
420	425	430
Val His Asp Gln Asn Ile Val His Ser Asp Leu Lys Pro Ala Asn Phe		
435	440	445
Leu Leu Val Glu Gly Asn Leu Lys Leu Ile Asp Phe Gly Ile Ala Lys		
450	455	460
Ala Ile Gly Asn Asp Thr Thr Asn Ile His Arg Asp Ser His Ile Gly		
465	470	475
		480

<210> 33
<211> 2263
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (379) . . . (1491)

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 Val Pro Phe Pro Ala Pro Ala Pro Pro Pro Gln Pro Pro Thr Pro Ala
 15 20 25

ctg ccg cac ccc ccg gcg cag ccg ccg ccg ccg ccc ccg cag cag ttc 507
 Leu Pro His Pro Pro Ala Gln Pro Pro Pro Pro Pro Pro Gln Gln Phe
 30 35 40

ccg cag ttc cac gtc aag tcc ggc ctg cag atc aag aag aac qcc atc 555

Pro Gln Phe His Val Lys Ser Gly Leu Gln Ile Lys Lys Asn Ala Ile			
45	50	55	
atc gat gac tac aag gtc acc agc cag gtc ctg ggg ctg ggc atc aac			603
Ile Asp Asp Tyr Lys Val Thr Ser Gln Val Leu Gly Leu Gly Ile Asn			
60	65	70	75
ggc aaa gtt ttg cag atc ttc aac aag agg acc cag gag aaa ttc gcc			651
Gly Lys Val Leu Gln Ile Phe Asn Lys Arg Thr Gln Glu Lys Phe Ala			
80	85	90	
ctc aaa atg ctt cag gac tgc ccc aag gcc cgc agg gag gtg gag ctg			699
Leu Lys Met Leu Gln Asp Cys Pro Lys Ala Arg Arg Glu Val Glu Leu			
95	100	105	
cac tgg cgg gcc tcc cag tgc ccg cac atc gta cgg atc gtg gat gtg			747
His Trp Arg Ala Ser Gln Cys Pro His Ile Val Arg Ile Val Asp Val			
110	115	120	
tac gag aat ctg tac gca ggg agg aag tgc ctg ctg att gtc atg gaa			795
Tyr Glu Asn Leu Tyr Ala Gly Arg Lys Cys Leu Leu Ile Val Met Glu			
125	130	135	
tgt ttg gac ggt gga gaa ctc ttt agc cga atc cag gat cga gga gac			843
Cys Leu Asp Gly Gly Glu Leu Phe Ser Arg Ile Gln Asp Arg Gly Asp			
140	145	150	155
cag gca ttc aca gaa aga gaa gca tcc gaa atc atg aag agc atc ggt			891
Gln Ala Phe Thr Glu Arg Glu Ala Ser Glu Ile Met Lys Ser Ile Gly			
160	165	170	
gag gcc atc cag tat ctg cat tca atc aac att gcc cat cgg gat gtc			939
Glu Ala Ile Gln Tyr Leu His Ser Ile Asn Ile Ala His Arg Asp Val			
175	180	185	
aag cct gag aat ctc tta tac acc tcc aaa agg ccc aac gcc atc ctg			987
Lys Pro Glu Asn Leu Leu Tyr Thr Ser Lys Arg Pro Asn Ala Ile Leu			
190	195	200	
aaa ctc act gac ttt ggc ttt gcc aag gaa acc acc agc cac aac tct			1035
Lys Leu Thr Asp Phe Gly Phe Ala Lys Glu Thr Thr Ser His Asn Ser			
205	210	215	
ttg acc act cct tgt tat aca ccg tac tat gtg gct cca gaa gtg ctg			1083
Leu Thr Thr Pro Cys Tyr Thr Pro Tyr Tyr Val Ala Pro Glu Val Leu			
220	225	230	235
ggt cca gag aag tat gac aag tcc tgt gac atg tgg tcc ctg ggt gtc			1131
Gly Pro Glu Lys Tyr Asp Lys Ser Cys Asp Met Trp Ser Leu Gly Val			
240	245	250	
atc atg tac atc ctg ctg tgt ggg tat ccc ccc ttc tac tcc aac cac			1179
Ile Met Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Ser Asn His			
255	260	265	
ggc ctt gcc atc tct ccg ggc atg aag act cgc atc cga atg ggc cag			1227
Gly Leu Ala Ile Ser Pro Gly Met Lys Thr Arg Ile Arg Met Gly Gln			

270	275	280	
tat gaa ttt ccc aac cca gaa tgg tca gaa gta tca gag gaa gtg aag Tyr Glu Phe Pro Asn Pro Glu Trp Ser Glu Val Ser Glu Glu Val Lys			
285	290	295	1275
atg ctc att cgg aat ctg ctg aaa aca gag ccc acc cag aga atg acc Met Leu Ile Arg Asn Leu Leu Lys Thr Glu Pro Thr Gln Arg Met Thr			
300	305	310	1323
315			
atc acc gag ttt atg aac cac cct tgg atc atg caa tca aca aag gtc Ile Thr Glu Phe Met Asn His Pro Trp Ile Met Gln Ser Thr Lys Val			
320	325	330	1371
cct caa acc cca ctg cac acc agc cgg gtc ctg aag gag gac aag gag Pro Gln Thr Pro Leu His Thr Ser Arg Val Leu Lys Glu Asp Lys Glu			
335	340	345	1419
cgg tgg gag gat gtc aag ggg tgt ctt cat gac aag aac agc gac cag Arg Trp Glu Asp Val Lys Gly Cys Leu His Asp Lys Asn Ser Asp Gln			
350	355	360	1467
gcc act tgg ctg acc agg ttg tga gcagaggatt ctgtttcct gtccaaactc 1521 Ala Thr Trp Leu Thr Arg Leu *			
365	370		
agtgcgttt cttagaatcc ttttattccc tgggtctcta atggacatt aaagaccatc 1581 tggtatcatc ttctcatttt gcagaagaga aactgaggcc cagaggcggg gggcagtctg 1641 ctcaaggta cgcagctggt gactgggtgg ggcagaccgg acccagggtt cctgactcct 1701 ggcccaagtc tcttcctcct atcctgcggg atcaactgggg ggctctcagg gaacagcagc 1761 agtgcctatc ccaggctctc tgctgcccag cgctggggtg aggctgcgtg tgtcagcgtg 1821 gaccactaac cagcccgctc tctctctctg ctccccacccc tgccgcctc accctgcct 1881 tgttgtctc gtctctcacg tctctttct gctgtctctc ctacctgtct tctggctctc 1941 tctgtaccct tcctgggtgt gccgtgcccc caggaggaga tgaccagtgc cttggccaca 2001 atgcgcgttg actacgagca gatcaagata aaaaagattt aagatgcata caaccctctg 2061 ctgctgaaga ggcggaaagaa agctcgggcc ctggaggctg cggctctggc ccactgagcc 2121 accgcgcctt cctgcccacg ggaggacaag caataactct ctacaggaat atattttta 2181 aacgaagaga cagaactgtc cacatctgcc tcctctcctc ctcagctgca tggagcctgg 2241 aactgcata gtgactgaat tc 2263			
<210> 34			
<211> 370			
<212> PRT			
<213> Homo sapiens			
<400> 34			
Met Leu Ser Asn Ser Gln Gly Gln Ser Pro Pro Val Pro Phe Pro Ala			
1	5	10	15
Pro Ala Pro Pro Pro Gln Pro Pro Thr Pro Ala Leu Pro His Pro Pro			
20	25	30	
Ala Gln Pro Pro Pro Pro Pro Gln Gln Phe Pro Gln Phe His Val			
35	40	45	
Lys Ser Gly Leu Gln Ile Lys Lys Asn Ala Ile Ile Asp Asp Tyr Lys			
50	55	60	
Val Thr Ser Gln Val Leu Gly Leu Gly Ile Asn Gly Lys Val Leu Gln			
65	70	75	80
Ile Phe Asn Lys Arg Thr Gln Glu Lys Phe Ala Leu Lys Met Leu Gln			

	85	90	95
Asp Cys Pro Lys Ala Arg Arg Glu Val Glu Leu His Trp Arg Ala Ser			
100	105	110	
Gln Cys Pro His Ile Val Arg Ile Val Asp Val Tyr Glu Asn Leu Tyr			
115	120	125	
Ala Gly Arg Lys Cys Leu Leu Ile Val Met Glu Cys Leu Asp Gly Gly			
130	135	140	
Glu Leu Phe Ser Arg Ile Gln Asp Arg Gly Asp Gln Ala Phe Thr Glu			
145	150	155	160
Arg Glu Ala Ser Glu Ile Met Lys Ser Ile Gly Glu Ala Ile Gln Tyr			
165	170	175	
Leu His Ser Ile Asn Ile Ala His Arg Asp Val Lys Pro Glu Asn Leu			
180	185	190	
Leu Tyr Thr Ser Lys Arg Pro Asn Ala Ile Leu Lys Leu Thr Asp Phe			
195	200	205	
Gly Phe Ala Lys Glu Thr Thr Ser His Asn Ser Leu Thr Thr Pro Cys			
210	215	220	
Tyr Thr Pro Tyr Tyr Val Ala Pro Glu Val Leu Gly Pro Glu Lys Tyr			
225	230	235	240
Asp Lys Ser Cys Asp Met Trp Ser Leu Gly Val Ile Met Tyr Ile Leu			
245	250	255	
Leu Cys Gly Tyr Pro Pro Phe Tyr Ser Asn His Gly Leu Ala Ile Ser			
260	265	270	
Pro Gly Met Lys Thr Arg Ile Arg Met Gly Gln Tyr Glu Phe Pro Asn			
275	280	285	
Pro Glu Trp Ser Glu Val Ser Glu Glu Val Lys Met Leu Ile Arg Asn			
290	295	300	
Leu Leu Lys Thr Glu Pro Thr Gln Arg Met Thr Ile Thr Glu Phe Met			
305	310	315	320
Asn His Pro Trp Ile Met Gln Ser Thr Lys Val Pro Gln Thr Pro Leu			
325	330	335	
His Thr Ser Arg Val Leu Lys Glu Asp Lys Glu Arg Trp Glu Asp Val			
340	345	350	
Lys Gly Cys Leu His Asp Lys Asn Ser Asp Gln Ala Thr Trp Leu Thr			
355	360	365	
Arg Leu			
370			

<210> 35
<211> 1074
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (628) ... (831)

<400> 35
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caaatcattc tgtaaccac cattccaaca ggtcgaggag agcttaaaca ccttcttcct 120
ctgccttgg tctatttttt tatttttg catcagtatt aatgttttg catactctcc 180
atcttatcc aaaaatgtaa acttcctttg tcaatctatg gatatgccca tatatgaaag 240
agatgggtgg gtcaaaaagg gatatcaa atgatgtatgg gggtcacaat gggaaatgg 300
aagtggtaaa taacattgcc aaaataatgt gccactagaa atgggtaaa ggctgtctt 360
tttttaaga aaagttatta ccatgtattt tgtgaggcag gtttacaaca ctacaagtct 420
tgactaagaa ggaaagagga aaaaagaaaa aacaccaata cccatattta aaaaaaaaaa 480

aatgatcata gtcttaggag ttcatataaa ccataggaac ttttactta tctcatgtta 540
ggtgtaccag tcagtgatta agtagaacta caagttatat aggctgtatt gtttattgtct 600
ggtttatgac cttaataaaat tgtaatt atg tat tac cag cag ggt gtt ttt aac 654
Met Tyr Tyr Gln Gln Gly Val Phe Asn
1 5

tgt gac tat tgt ata aaa aca aat ctt gat atc cag aag cac atg aag 702
Cys Asp Tyr Cys Ile Lys Thr Asn Leu Asp Ile Gln Lys His Met Lys
10 15 20 25

ttt gcg act ttc cac cct gcc cat ttt tgt aaa act gca gtc atc ttg 750
Phe Ala Thr Phe His Pro Ala His Phe Cys Lys Thr Ala Val Ile Leu
30 35 40

gac ctt tta aac aca aat ttt aaa ctc aac caa gct gtg ata agc gga 798
Asp Leu Leu Asn Thr Asn Phe Lys Leu Asn Gln Ala Val Ile Ser Gly .
45 50 55

atg gtt act gtt tat act gtg gta tgt ttt tga ttacagcaga taatgcttc 851
Met Val Thr Val Tyr Thr Val Val Cys Phe *
60 65

ttttccagtc atcttgaga ataaaggaaa aaaaaaatct tcagatgcaa tggtttgc 911
tagcatcttg tctatcatgt tttgtaaatg ctggagaagc gtcgaccaat ttgacttaga 971
gatggaatgt aactttgctt acaaaaattg ctattaaact cctacttaag gtgttcta 1031
tttctgtgag cacactaaaa acaaaaatat atgtgaataa aat 1074

<210> 36

<211> 67

<212> PRT

<213> Homo sapiens

<400> 36

Met Tyr Tyr Gln Gln Gly Val Phe Asn Cys Asp Tyr Cys Ile Lys Thr
1 5 10 15
Asn Leu Asp Ile Gln Lys His Met Lys Phe Ala Thr Phe His Pro Ala
20 25 30
His Phe Cys Lys Thr Ala Val Ile Leu Asp Leu Leu Asn Thr Asn Phe
35 40 45
Lys Leu Asn Gln Ala Val Ile Ser Gly Met Val Thr Val Tyr Thr Val
50 55 60
Val Cys Phe
65

<210> 37

<211> 1356

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (553)...(1095)

<400> 37

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ctccccccct cacgcccccc ctctcgccctt cgccgaacca aagtggatta attacacgct 120

ttctgtttct ctccgtgctg ttctctcccc ctgtgcgcct gcccgcctct cgctgtcctc 180
 tctccccctc gcccctctctt cggccccccc ctttacgtt cactctgtct cteccactat 240
 ctctgccccctt ctctatcctt gataacaacag ctgacacctt ttcccgataac cttttcccccc 300
 ccgaaaaagta caacatctgg cccgccccag cccgaagaca gcccgtcctc cctggacaat 360
 cagacgaatt ctccccccccccc ccccaaaaaaa aaaagccatc ccccccgtct gccccgtcgc 420
 acattcggcc cccgcgactc ggccagagcg ggcgtggcag aggagtgtcc ggcaggaggg 480
 ccaacgccccctt ctgttcgggtt tgcgacacgc agcagggagg tgggcggcag cgtcgccggc 540
 ttccagacac ca atg gga atc cca atg ggg aag tcg atg ctg gtg ctt ctc 591
 Met Gly Ile Pro Met Gly Lys Ser Met Leu Val Leu Leu
 1 5 10

acc	ttc	ttg	gcc	tcc	gcc	tcg	tgc	tgc	att	gct	gct	tac	cgc	ccc	agt	639
Thr	Phe	Leu	Ala	Phe	Ala	Ser	Cys	Cys	Ile	Ala	Ala	Tyr	Arg	Pro	Ser	
15																25

gag	acc	ctg	tgc	ggc	ggg	gag	ctg	gtg	gac	acc	ctc	cag	ttc	gtc	tgt	687
Glu	Thr	Leu	Cys	Gly	Gly	Glu	Leu	Val	Asp	Thr	Leu	Gln	Phe	Val	Cys	
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ggg	gac	cgc	ggc	ttc	tac	ttc	agc	agg	ccc	gca	agc	cgt	gtg	agc	cgt	735
Gly	Asp	Arg	Gly	Phe	Tyr	Phe	Ser	Arg	Pro	Ala	Ser	Arg	Val	Ser	Arg	
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cgc	agc	cgt	ggc	atc	gtt	gag	gag	tgc	tgt	ttc	cgc	agc	tgt	gac	ctg	783
Arg	Ser	Arg	Gly	Ile	Val	Glu	Glu	Cys	Cys	Phe	Arg	Ser	Cys	Asp	Leu	
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gcc	ctc	ctg	gag	acg	tac	tgt	gct	acc	ccc	gcc	aag	tcc	gag	agg	gac	831
Ala	Leu	Leu	Glu	Thr	Tyr	Cys	Ala	Thr	Pro	Ala	Lys	Ser	Glu	Arg	Asp	
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gtg	tcg	acc	cct	ccg	acc	gtg	ctt	ccg	gac	aac	ttc	ccc	aga	tac	ccc	879
Val	Ser	Thr	Pro	Pro	Thr	Val	Leu	Pro	Asp	Asn	Phe	Pro	Arg	Tyr	Pro	
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gtg	ggc	aag	ttc	ttc	caa	tat	gac	acc	tgg	aag	cag	tcc	acc	cag	cgc	927
Val	Gly	Lys	Phe	Phe	Gln	Tyr	Asp	Thr	Trp	Lys	Gln	Ser	Thr	Gln	Arg	
110																125

ctg	cgc	agg	ggc	ctg	cct	gcc	ctc	ctg	cgt	gcc	cgc	cg	gg	cat	gtg	975
Leu	Arg	Arg	Gly	Leu	Pro	Ala	Leu	Leu	Arg	Ala	Arg	Arg	Gly	His	Val	
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ctc	gcc	aag	gag	ctc	gag	gcf	ttc	agg	gag	gcc	aaa	cgt	cac	cgt	ccc	1023
Leu	Ala	Lys	Glu	Leu	Ala	Phe	Arg	Glu	Ala	Lys	Arg	His	Arg	Pro		
145																155

ctg	att	gct	cta	ccc	acc	caa	gac	ccc	gcc	cac	ggg	ggc	gcc	ccc	cca	1071
Leu	Ile	Ala	Leu	Pro	Thr	Gln	Asp	Pro	Ala	His	Gly	Gly	Ala	Pro	Pro	
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gag	atg	gcc	agc	aat	cgg	aag	tga	gcaaaaactgc	cgcaagtctg	cagccggc	1125					
Glu	Met	Ala	Ser	Asn	Arg	Lys	*									
175																180

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35 40 45
Gly Phe Tyr Phe Ser Arg Pro Ala Ser Arg Val Ser Arg Arg Ser Arg
50 55 60
Gly Ile Val Glu Glu Cys Cys Phe Arg Ser Cys Asp Leu Ala Leu Leu
65 70 75 80
Glu Thr Tyr Cys Ala Thr Pro Ala Lys Ser Glu Arg Asp Val Ser Thr
85 90 95
Pro Pro Thr Val Leu Pro Asp Asn Phe Pro Arg Tyr Pro Val Gly Lys
100 105 110
Phe Phe Gln Tyr Asp Thr Trp Lys Gln Ser Thr Gln Arg Leu Arg Arg
115 120 125
Gly Leu Pro Ala Leu Leu Arg Ala Arg Arg Gly His Val Leu Ala Lys
130 135 140
Glu Leu Glu Ala Phe Arg Glu Ala Lys Arg His Arg Pro Leu Ile Ala
145 150 155 160
Leu Pro Thr Gln Asp Pro Ala His Gly Ala Pro Pro Glu Met Ala
165 170 175
Ser Asn Arg Lys
180